

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry; Van den Eynde, Benoit; Van Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: 08/142,368
(B) FILING DATE: 02-MAY-1994
(C) CLASSIFICATION: 435
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: PCT/US92/04354
(B) FILING DATE: 22-MAY-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: 12-DECEMBER-1991
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/764,364
(B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/728,838
(b) FILING DATE: 9-JULY-1991
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/705,702
(B) FILING DATE: 23-May-1991
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 5253.4-US

00019669.031797

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 688-9200
(B) TELEFAX: (212) 838-3884

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCGCCT ACAGCTCTAG 180
CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGCG ACTCTACTCT 420
TATCTTA ACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
5 10 15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
20 25 30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
35 40 45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
50 55 60
TAT GAA AGG GAT GTG GCC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser

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65	TCT	GTC	GAT	GAG	GAT	GAA	GAC	GAT	GAG	GAT	GAT	GAG	GAT	GAC	TAC	TAC	288
	Ser	Val	Asp	Glu	Asp	Glu	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Asp	Tyr	Tyr	
					85					90					95		
	GAC	GAC	GAG	GAC	GAC	GAC	GAC	GAT	GCC	TTC	TAT	GAT	GAT	GAG	GAT	GAT	336
	Asp	Asp	Glu	Asp	Asp	Asp	Asp	Asp	Ala	Phe	Tyr	Asp	Asp	Glu	Asp	Asp	
					100					105					110		
	GAG	GAA	GAA	GAA	TTG	GAG	AAC	CTG	ATG	GAT	GAT	GAA	TCA	GAA	GAT	GAG	384
	Glu	Glu	Glu	Glu	Leu	Glu	Asn	Leu	Met	Asp	Asp	Glu	Ser	Glu	Asp	Glu	
					115					120					125		
	GCC	GAA	GAA	GAG	ATG	AGC	GTG	GAA	ATG	GGT	GCC	GGA	GCT	GAG	GAA	ATG	432
	Ala	Glu	Glu	Glu	Met	Ser	Val	Glu	Met	Gly	Ala	Gly	Ala	Glu	Glu	Met	
					130					135					140		
	GGT	GCT	GGC	GCT	AAC	TGT	GCC	TGT	GTT	CCT	GGC	CAT	CAT	TTA	AGG	AAG	480
	Gly	Ala	Gly	Ala	Asn	Cys	Ala	Cys	Val	Pro	Gly	His	His	Leu	Arg	Lys	
					145					150					155		
	AAT	GAA	GTG	AAG	TGT	AGG	ATG	ATT	TAT	TTC	TTC	CAC	GAC	CCT	AAT	TTC	528
	Asn	Glu	Val	Lys	Cys	Arg	Met	Ile	Tyr	Phe	Phe	His	Asp	Pro	Asn	Phe	
					165					170					175		
	CTG	GTG	TCT	ATA	CCA	GTG	AAC	CCT	AAG	GAA	CAA	ATG	GAG	TGT	AGG	TGT	576
	Leu	Val	Ser	Ile	Pro	Val	Asn	Pro	Lys	Glu	Gln	Met	Glu	Cys	Arg	Cys	
					180					185					190		
	GAA	AAT	GCT	GAT	GAA	GAG	GTT	GCA	ATG	GAA	GAG	GAA	GAA	GAA	GAA	GAG	624
	Glu	Asn	Ala	Asp	Glu	Glu	Val	Ala	Met	Glu	Glu	Glu	Glu	Glu	Glu	Glu	
					195					200					210		
	GAG	GAG	GAG	GAG	GAA	GAG	GAA	ATG	GGA	AAC	CCG	GAT	GGC	TTC	TCA	CCT	672
	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Met	Gly	Asn	Pro	Asp	Gly	Phe	Ser	Pro	
					220					225					230		
																235	
	TAG																675

(2) INFORMATION FOR SEQUENCE ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTtagt	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACCTT	CATATGATAC	180
ATAGGATTAC	ACTTGTACCT	GTTAAAAATA	AAAGTTTGAC	TTGCATAC		228

(2) INFORMATION FOR SEQUENCE ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1365 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG 350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
ACCCTTTGTG CC 462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
TAG 1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
TTGTTTTTTT TTCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

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(2) INFORMATION FOR SEQUENCE ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4698 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG	AATGAAAAGA	ACCCGGGACT	CCCAAAGACG	CTAGATGTGT	50
GAAGATCCTG	ATCACTCATT	GGGTGTCTGA	GTTCTGCGAT	ATTCATCCCT	100
CAGCCAATGA	GCTTACTGTT	CTCGTGGGGG	GTTTGTGAGC	CTTGGGTAGG	150
AAGTTTTGCA	AGTTCCGCCT	ACAGCTCTAG	CTTGTGAATT	TGTACCCTTT	200
CACGTAAAAA	AGTAGTCCAG	AGTTTACTAC	ACCCTCCCTC	CCCCCTCCCA	250
CCTCGTGCTG	TGCTGAGTTT	AGAAGTCTTC	CTTATAGAAG	TCTTCCGTAT	300
AGAACTCTTC	CGGAGGAAGG	AGGGAGGACC	CCCCCCTTTT	GCTCTCCAG	350
CATGCATTGT	GTCAACGCCA	TTGCACTGAG	CTGGTCGAAG	AAGTAAGCCG	400
CTAGCTTGCG	ACTCTACTCT	TATCTTAACT	TAGCTCGGCT	TCCTGCTGGT	450
ACCCTTTGTG	CC				462
ATG TCT GAT	AAC AAG AAA CCA	GAC AAA GCC CAC	AGT GGC TCA		504
GGT GGT GAC	GGT GAT GGG AAT	AGG TGC AAT TTA	TTG CAC CGG		546
TAC TCC CTG	GAA GAA ATT CTG	CCT TAT CTA GGG	TGG CTG GTC		588
TTC GCT GTT	GTC ACA ACA AGT	TTT CTG GCG CTC	CAG ATG TTC		630
ATA GAC GCC	CTT TAT GAG GAG	CAG TAT GAA AGG	GAT GTG GCC		672
TGG ATA GCC	AGG CAA AGC AAG	CGC ATG TCC TCT	GTC GAT GAG		714
GAT GAA GAC	GAT GAG GAT GAT	GAG GAT GAC TAC	TAC GAC GAC		756
GAG GAC GAC	GAC GAC GAT GCC	TTC TAT GAT GAT	GAG GAT GAT		798
GAG GAA GAA	GAA TTG GAG AAC	CTG ATG GAT GAT	GAA TCA GAA		840
GAT GAG GCC	GAA GAA GAG ATG	AGC GTG GAA ATG	GGT GCC GGA		882
GCT GAG GAA	ATG GGT GCT GGC	GCT AAC TGT GCC	T		916
GTGAGTAACC	CGTGGTCTTT	ACTCTAGATT	CAGGTGGGGT	GCATTCTTTA	966
CTCTTGCCCA	CATCTGTAGT	AAAGACCACA	TTTTGGTTGG	GGGTCATTGC	1016
TGGAGCCATT	CCTGGCTCTC	CTGTCCACGC	CTATCCCCGC	TCCTCCCATC	1066
CCCCACTCCT	TGCTCCGCTC	TCTTTCCTTT	TCCCACCTTG	CCTCTGGAGC	1116
TTCAGTCCAT	CCTGCTCTGC	TCCCTTTCCC	CTTTGCTCTC	CTTGCTCCCC	1166
TCCCCCTCGG	CTCAACTTTT	CGTGCCTTCT	GCTCTCTGAT	CCCCACCCTC	1216
TTCAGGCTTC	CCCATTGCT	CCTCTCCCGA	AACCCTCCCC	TTCCTGTTCC	1266
CCTTTTCGCG	CCTTTTCTTT	CCTGCTCCCC	TCCCCCTCCC	TATTTACCTT	1316
TCACCAGCTT	TGCTCTCCCT	GCTCCCCCTC	CCCTTTTGCA	CCTTTTCTTT	1366
TCCTGCTCCC	CTCCCCCTCC	CCTCCCTGTT	TACCCTTCAC	CGCTTTTCCT	1416
CTACCTGCTT	CCCTCCCCCT	TGCTGCTCCC	TCCCTATTG	CATTTTCGGG	1466
TGCTCCTCCC	TCCCCCTCCC	CCTCCCTCCC	TATTTGCATT	TTCGGGTGCT	1516
CCTCCCTCCC	CCTCCCCAGG	CCTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	1566
TTGGTTTTTC	GAGACAGGGT	TTCTCTTTGT	ATCCCTGGCT	GTCCTGGCAC	1616
TCACTCTGTA	GACCAGGCTG	GCCTCAAAC	CAGAAATCTG	CCTGCCTCTG	1666
CCTCCCAAAT	GCTGGGATTA	AAGGCTTGCA	CCAGGACTGC	CCCAGTGCAG	1716
GCCTTTCCTT	TTTCTCCTCT	CTGGTCTCCC	TAATCCCTTT	TCTGCATGTT	1766
AACTCCCCTT	TTGGCACCTT	TCCTTTACAG	GACCCCTCC	CCCTCCCTGT	1816
TTCCCTTCCG	GCACCCTTCC	TAGCCCTGCT	CTGTTCCCTC	TCCCTGCTCC	1866
CCTCCCCCTC	TTTGCTCGAC	TTTTAGCAGC	CTTACCTCTC	CCTGCTTTCT	1916
GCCCCGTTCC	CCTTTTTTGT	GCCTTTCCTC	CTGGCTCCCC	TCCACCTTCC	1966
AGCTCACCTT	TTTGTTTGT	TGGTTGTTG	GTTGTTTGGT	TTGCTTTTTT	2016
TTTTTTTTTT	GCACCTTGTT	TTCCAAGATC	CCCCTCCCCC	TCCGGCTTCC	2066
CCTCTGTGTG	CCTTTCCTGT	TCCCTCCCCC	TCGCTGGCTC	CCCCTCCCTT	2116

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TCTGCCTTTC	CTGTCCCTGC	TCCCTTCTCT	GCTAACCTTT	TAATGCCTTT	2166
CTTTTCTAGA	CTCCCCCCTC	CAGGCTTGCT	GTTTGCTTCT	GTGCACTTTT	2216
CCTGACCCTG	CTCCCCCTTC	CCTCCCAGCT	CCCCCTCTT	TTCCCACCTC	2266
CCTTTCTCCA	GCCTGTCACC	CCTCCTTCTC	TCCTCTCTGT	TTCTCCCACT	2316
TCCTGCTTCC	TTTACCCCTT	CCCTCTCCCT	ACTCTCCTCC	CTGCCTGCTG	2366
GACTTCCTCT	CCAGCCGCCC	AGTTCCTGCG	AGTCCTGGAG	TCTTTCCTGC	2416
CTCTCTGTCC	ATCACTTCCC	CCTAGTTTCA	CTTCCCTTTC	ACTCTCCCCT	2466
ATGTGTCTCT	CTTCCTATCT	ATCCCTTCCT	TTCTGTCCCC	TCTCCTCTGT	2516
CCATCACCTC	TCTCCTCCCT	TCCCTTTCCT	CTCTCTTCCA	TTTTCTTCCA	2566
CCTGCTTCTT	TACCCTGCCT	CTCCCATTGC	CCTCTTACCT	TTATGCCCCAT	2616
TCCATGTCCC	CTCTCAATTC	CCTGTCCCAT	TGTGCTCCCT	CACATCTTCC	2666
ATTTCCCTCT	TTCTCCCTTA	GCCTCTTCTT	CCTCTTCTCT	TGTATCTCCC	2716
TTCCCTTTGC	TTCTCCCTCC	TCCTTTCCCC	TTCCCTATG	CCCTCTACTC	2766
TACTTGATCT	TCTCTCCTCT	CCACATACCC	TTTTTCCTTT	CCACCCTGCC	2816
CTTTGTCCCC	AGACCCTACA	GTATCCTGTG	CACAGGAAGT	GGGAGGTGCC	2866
ATCAACAACA	AGGAGGCAAG	AAACAGAGCA	AAATCCCCAA	ATCAGCAGGA	2916
AAGGCTGGAT	GAAAATAAGG	CCAGGTTCTG	AGGACAGCTG	GAATCTAGCC	2966
AAGTGGCTCC	TATAACCCTA	AGTACCAAGG	GAGAAAGTGA	TGGTGAAGTT	3016
CTTGATCCTT	GCTGCTTCTT	TTACATATGT	TGGCACATCT	TTCTCAAATG	3066
CAGGCCATGC	TCCATGCTTG	GCGCTTGCTC	AGCGTGGTTA	AGTAATGGGA	3116
GAATCTGAAA	ACTAGGGGCC	AGTGGTTTGT	TTTGGGGACA	AATTAGCACG	3166
TAGTGATATT	TCCCCCTAAA	AATTATAACA	AACAGATTCA	TGATTTGAGA	3216
TCCTTCTACA	GGTGAGAAGT	GGAAAAATTG	TCACTATGAA	GTTCTTTTTA	3266
GGCTAAAGAT	ACTTGGAACC	ATAGAAGCGT	TGTTAAAATA	CTGCTTTCTT	3316
TTGCTAAAAT	ATTCTTTCTC	ACATATTTCAT	ATTCTCCAG		3355
GT GTT CCT	GGC CAT CAT	TTA AGG AAG	AAT GAA GTG	AAG TGT	3396
AGG ATG ATT	TAT TTC TTC	CAC GAC CCT	AAT TTC CTG	GTG TCT	3438
ATA CCA GTG	AAC CCT AAG	GAA CAA ATG	GAG TGT AGG	TGT GAA	3480
AAT GCT GAT	GAA GAG GTT	GCA ATG GAA	GAG GAA GAA	GAA GAA	3522
GAG GAG GAG	GAG GAG GAA	GAG GAA ATG	GGA AAC CCG	GAT GGC	3564
TTC TCA CCT	TAG				3576
GCATGCAGGT	ACTGGCTTCA	CTAACCAACC	ATTCCTAACA	TATGCCTGTA	3626
GCTAAGAGCA	TCTTTTAA	AAATATTATT	GGTAAACTAA	ACAATTGTTA	3676
TCTTTTACA	TTAATAAGTA	TTAAATTAAT	CCAGTATACA	GTTTTAAGAA	3726
CCCTAAGTTA	AACAGAAGTC	AATGATGTCT	AGATGCCTGT	TCTTTAGATT	3776
GTAGTGAGAC	TACTTACTAC	AGATGAGAAG	TTGTTAGACT	CGGGAGTAGA	3826
GACCAGTAAA	AGATCATGCA	GTGAAATGTG	GCCATGGAAA	TCGCATATTG	3876
TTCTTATAGT	ACCTTTGAGA	CAGCTGATAA	CAGCTGACAA	AAATAAGTGT	3926
TTCAAGAAAG	ATCACACGCC	ATGGTTCACA	TGCAAATTAT	TATTTTGTCTG	3976
TTCTGATTTT	TTTCATTTCT	AGACCTGTGG	TTTTAAAGAG	ATGAAAATCT	4026
CTTAAAATTT	CCTTCATCTT	TAATTTTCCT	TAACTTTAGT	TTTTTTCACT	4076
TAGAATTCAA	TTCAAATTCT	TAATTCAATC	TTAATTTTAA	GATTTCCTAA	4126
AATGTTTTTT	AAAAAAAATG	CAAATCTCAT	TTTTAAGAGA	TGAAAGCAGA	4176
GTAACCTGGG	GGCTTAGGGA	ATCTGTAGGG	TTGCGGTATA	GCAATAGGGA	4226
GTTCTGGTCT	CTGAGAAGCA	GTCAGAGAGA	ATGGAAAACC	AGGCCCTTGC	4276
CAGTAGGTTA	GTGAGGTTGA	TATGATCAGA	TTATGGACAC	TCTCCAAATC	4326
ATAAATACTC	TAACAGCTAA	GGATCTCTGA	GGGAAACACA	ACAGGGAAAT	4376
ATTTTAGTTT	CTCCTTGAGA	AACAATGACA	AGACATAAAA	TTGGCAAGAA	4426
AGTCAGGAGT	GTATTCTAAT	AAGTGTTGCT	TATCTCTTAT	TTTCTTCTAC	4476
AGTTGCAAAG	CCCAGAAGAA	AGAAATGGAC	AGCGGAAGAA	GTGGTTGTTT	4526
TTTTTTCCCC	TTCATTAATT	TTCTAGTTTT	TAGTAATCCA	GAAAATTTGA	4576
TTTTGTTCTA	AAGTTCATTA	TGCAAAGATG	TCACCAACAG	ACTTCTGACT	4626
GCATGGTGAA	CTTTCATATG	ATACATAGGA	TTACACTTGT	ACCTGTTAAA	4676
AATAAAAGTT	TGACTTGCA	TAC			4698

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: protein
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe
 5

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2419 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCACT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCCGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCCTCCTTC	AGGTTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTTCAG	TTCTCAGCTG	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCC	AACAAGAGGC	CCTGGGCCTG	700
GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCCTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
TGTTTGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCCTGA	1050
GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCACCC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
TTTGGTGCAG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCGG	ACAGTGATCC	1400

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CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT	CCCTGCGTGA	AGCAGCTTTG	AGAGAGGAGG	AAGAGGGAGT	1550
CTGAGCATGA	GTTGCAGCCA	AGGCCAGTGG	GAGGGGGACT	GGGCCAGTGC	1600
ACCTTCCAGG	GCCGCGTCCA	GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA	GAGCGGTCAG	TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG	GGTGACTTGG	AGATTTATCT	TTGTTCTCTT	TTGGAATTGT	1750
TCAAATGTTT	TTTTTTAAGG	GATGGTTGAA	TGAACTTCAG	CATCCAAGTT	1800
TATGAATGAC	AGCAGTCACA	CAGTTCTGTG	TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTTG	TTATTTCAGAT	TGGGAAATCC	ATTCTATTTT	GTGAATTGGG	1900
ATAATAACAG	CAGTGGAATA	AGTACTTAGA	AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA	GATAAAGAAC	TAAAGAAATT	AAGAGATAGT	CAATTCTTGC	2000
CTTATACCTC	AGTCTATTCT	GTAAAATTTT	TAAAGATATA	TGCATACCTG	2050
GATTTCCCTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100
AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2419

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5674 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCGGGGCAC	CACTGGCATC	CCTCCCCCTA	CCACCCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGAGGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCCAG	CCCCCTTGCT	GCTTAAACCA	400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGCTTAGG	450
AGAGGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
ATGCTCACTC	CCGTGACCCA	ACCCCCTCTT	CATTGTCAAT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
ATTCCACCCT	CACCCCCACC	CCCACCCCCA	CGCCCACTCC	CACCCCCACC	700
CAGGCAGGAT	CCGGTTCCCC	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800
AGGGACGGCG	TAGAGTTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
AGGCAAGGTG	AGAGGCTGAG	GGAGGACTGA	GGACCCCGCC	ACTCCAAATA	900

GAGAGCCCCA	AATATTCCAG	CCCCGCCCTT	GCTGCCAGCC	CTGGCCCACC	950
CGCGGGAAGA	CGTCTCAGCC	TGGGCTGCCC	CCAGACCCCT	GCTCCAAAAG	1000
CCTTGAGAGA	CACCAGGTTT	TTCTCCCCAA	GCTCTGGAAT	CAGAGGTTGC	1050
TGTGACCAGG	GCAGGACTGG	TTAGGAGAGG	GCAGGGCACA	GGCTCTGCCA	1100
GGCATCAAGA	TCAGCACCCA	AGAGGGAGGG	CTGTGGGCCC	CCAAGACTGC	1150
ACTCCAATCC	CCACTCCCAC	CCCATTTCGA	TTCCCATTC	CCACCCAACC	1200
CCCATCTCCT	CAGCTACACC	TCCACCCCCA	TCCCTACTCC	TACTCCGTCA	1250
CCTGACCACC	ACCCTCCAGC	CCCAGCACCA	GCCCCAACCC	TTCTGCCACC	1300
TCACCCTCAC	TGCCCCCAAC	CCCACCCTCA	TCTCTCTCAT	GTGCCCCACT	1350
CCCATCGCCT	CCCCCATTC	GGCAGAATCC	GGTTTGCCCC	TGCTCTCAAC	1400
CCAGGGAAGC	CCTGGTAGGC	CCGATGTGAA	ACCACTGACT	TGAACCTCAC	1450
AGATCTGAGA	GAAGCCAGGT	TCATTTAATG	GTTCTGAGGG	GCGGCTTGAG	1500
ATCCACTGAG	GGGAGTGTTT	TTAGGCTCTG	TGAGGAGGCA	AGGTGAGATG	1550
CTGAGGGAGG	ACTGAGGAGG	CACACACCCC	AGGTAGATGG	CCCCAAAATG	1600
ATCCAGTACC	ACCCCTGCTG	CCAGCCCTGG	ACCACCCGGC	CAGGACAGAT	1650
GTCTCAGCTG	GACCACCCCC	CGTCCCGTCC	CACTGCCACT	TAACCCACAG	1700
GGCAATCTGT	AGTCATAGCT	TATGTGACCG	GGGCAGGGTT	GGTCAGGAGA	1750
GGCAGGGCCC	AGGCATCAAG	GTCCAGCATC	CGCCCGGCAT	TAGGGTCAGG	1800
ACCCTGGGAG	GGAAGTGAGG	GTTCCCCACC	CACACCTGTC	TCCTCATCTC	1850
CACCGCCACC	CCACTCACAT	TCCCATACTT	ACCCCTTACC	CCCAACCTCA	1900
TCTTGTCAGA	ATCCCTGCTG	TCAACCCACG	GAAGCCACGG	GAATGGCGGC	1950
CAGGCACTCG	GATCTTGACG	TCCCCATCCA	GGGTCTGATG	GAGGGAAGGG	2000
GCTTGAACAG	GGCCTCAGGG	GAGCAGAGGG	AGGGCCCTAC	TGCGAGATGA	2050
GGGAGGCCTC	AGAGGACCCA	GCACCCTAGG	ACACCGCACC	CCTGTCTGAG	2100
ACTGAGGCTG	CCACTTCTGG	CCTCAAGAAT	CAGAACGATG	GGGACTCAGA	2150
TTGCATGGGG	GTGGGACCCA	GGCCTGCAAG	GCTTACGCGG	AGGAAGAGGA	2200
GGGAGGACTC	AGGGGACCTT	GGAATCCAGA	TCAGTGTGGA	CCTCGGCCCT	2250
GAGAGGTCCA	GGGCACGGTG	GCCACATATG	GCCCATATTT	CCTGCATCTT	2300
TGAGGTGACA	GGACAGAGCT	GTGGTCTGAG	AAGTGGGGCC	TCAGGTCAAC	2350
AGAGGGAGGA	GTTCCAGGAT	CCATATGGCC	CAAGATGTGC	CCCCTTCATG	2400
AGGACTGGGG	ATATCCCCGG	CTCAGAAAGA	AGGGACTCCA	CACAGTCTGG	2450
CTGTCCCCTT	TTAGTAGCTC	TAGGGGGACC	AGATCAGGGA	TGGCGGTATG	2500
TTCCATTCTC	ACTTGATACC	CAGGCAGGAA	GTTGGGGGGC	CCTCAGGGAG	2550
ATGGGGTCTT	GGGGTAAAGG	GGGGATGTCT	ACTCATGTCA	GGGAATTGGG	2600
GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTGAGC	CCTGGACACC	2700
TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCCAG	GACCAGAACA	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCCAGAG	AGCATGGGCT	2950
GGGCCGTCTG	CCGAGGTCCT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCTCCTT	GTCCTTCCAT	3200
TCCTTATCAT	GGATGTGAAC	TCTTGATTTG	GATTTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
CACCCCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
CTGAGGGCCC	GTGGATTCCCT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600

TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
CTCACTTCCT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
ATTCCCTGGA	GGCCACAGAG	GAGCACC AAG	GAGAAGATCT	GTAAGTAGGC	3750
CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCACA	3850
CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG CCT	GAG GAA	3922
GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG GTG	TGT GTG	3964
CAG GCT GCC	ACC TCC TCC	TCT CCT CTG	GTC CTG GGC	ACC	4006
CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT CCT	CCC CAG	4048
AGT CCT CAG	GGA GCC TCC	GCC TTT CCC	ACT ACC ATC	AAC TTC	4090
ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC AGC	CGT GAA	4132
GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG TCC	TTG TTC	4174
CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG GTT	GGT TTT	4216
CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC ACA	AAG GCA	4258
GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG CAC	TGT TTT	4300
CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG CAG	CTG GTC	4342
TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC GGC	CAC TCC	4384
TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT GAT	GGC CTG	4426
CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC TTC	CTG ATA	4468
ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC CAT	GCT CCT	4510
GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG GAG	GTG TAT	4552
GAT GGG AGG	GAG CAC AGT	GCC TAT GGG	GAG CCC AGG	AAG CTG	4594
CTC ACC CAA	GAT TTG GTG	CAG GAA AAG	TAC CTG GAG	TAC GGC	4636
AGG TGC CGG	ACA GTG ATC	CCG CAC GCT	ATG AGT TCC	TGT GGG	4678
GTC CAA GGG	CCC TCG CTG	AAA CCA GCT	ATG TGA		4711
AAGTCCTTGA	GTATGTGATC	AAGGTCAGTG	CAAGAGTTC		4750
GCTTTTTTCTT	CCCATCCCTG	CGTGAAGCAG	CTTTGAGAGA	GGAGGAAGAG	4800
GGAGTCTGAG	CATGAGTTGC	AGCCAAGGCC	AGTGGGAGGG	GGACTGGGCC	4850
AGTGCACCTT	CCAGGGCCGC	GTCCAGCAGC	TTCCCCTGCC	TCGTGTGACA	4900
TGAGGCCCAT	TCTTCACTCT	GAAGAGAGCG	GTCAGTGTTT	TCAGTAGTAG	4950
GTTTCTGTTC	TATTGGGTGA	CTTGGAGATT	TATCTTTGTT	CTCTTTTGGA	5000
ATTGTTCAAA	TGTTTTTTTT	TAAGGGATGG	TTGAATGAAC	TTCAGCATCC	5050
AAGTTTATGA	ATGACAGCAG	TCACACAGTT	CTGTGTATAT	AGTTTAAGGG	5100
TAAGAGTCTT	GTGTTTTTAT	CAGATTGGGA	AATCCATTCT	ATTTTGTGAA	5150
TTGGGATAAT	AACAGCAGTG	GAATAAGTAC	TTAGAAATGT	GAAAAATGAG	5200
CAGTAAAATA	GATGAGATAA	AGA ACTAAAG	AAATTAAGAG	ATAGTCAATT	5250
CTTGCCTTAT	ACCTCAGTCT	ATTCTGTAAA	ATTTTAAAG	ATATATGCAT	5300
ACCTGGATTT	CCTTGGCTTC	TTTGAGAATG	TAAGAGAAAT	TAAATCTGAA	5350
TAAAGAATTC	TTCTGTTC	CTGGCTCTTT	TCTTCTCCAT	GCACTGAGCA	5400
TCTGCTTTTT	GGAAGGCCCT	GGGTTAGTAG	TGGAGATGCT	AAGGTAAGCC	5450
AGACTCATAC	CCACCCATAG	GGTCGTAGAG	TCTAGGAGCT	GCAGTCACGT	5500
AATCGAGGTG	GCAAGATGTC	CTCTAAAGAT	GTAGGGAAAA	GTGAGAGAGG	5550
GGTGAGGGTG	TGGGGCTCCG	GGTGAGAGTG	GTGGAGTGTC	AATGCCCTGA	5600
GCTGGGGCAT	TTTGGGCTTT	GGGAAACTGC	AGTTCCTTCT	GGGGGAGCTG	5650
ATTGTAATGA	TCTTGGGTGG	ATCC			5674

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucl ic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACC GCAG	350
GGA ACTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTCAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCACTG	TACCCCTGTC	800
TCAA ACTGAG	CCACCTTTTC	ATT CAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCC ACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGAGGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTCAGGG	1300
GGT TCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTT CACCCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
GTCTTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTG GG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050

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CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTC	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCCGACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723
TCT ACT CTA	GTG GAA GTT	ACC CTG GGG	GAG GTG CCT	GCT GCC	2765
GAC TCA CCG	AGT CCT CCC	CAC AGT CCT	CAG GGA GCC	TCC AGC	2807
TTC TCG ACT	ACC ATC AAC	TAC ACT CTT	TGG AGA CAA	TCC GAT	2849
GAG GGC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGA	ATG TTT	2891
CCC GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA ATC AGT	AGG AAG	2933
ATG GTT GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	2975
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GAG AGT	GTC CTC	3017
AGA AAT TGC	CAG GAC TTC	TTT CCC GTG	ATC TTC AGC	AAA GCC	3059
TCC GAG TAC	TTG CAG CTG	GTC TTT GGC	ATC GAG GTG	GTG GAA	3101
GTG GTC CCC	ATC AGC CAC	TTG TAC ATC	CTT GTC ACC	TGC CTG	3143
GGC CTC TCC	TAC GAT GGC	CTG CTG GGC	GAC AAT CAG	GTC ATG	3185
CCC AAG ACA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	3227
ATA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	3269
CTG AGT ATG	TTG GAG GTG	TTT GAG GGG	AGG GAG GAC	AGT GTC	3311
TTC GCA CAT	CCC AGG AAG	CTG CTC ATG	CAA GAT CTG	GTG CAG	3353
GAA AAC TAC	CTG GAG TAC	CGG CAG GTG	CCC GGC AGT	GAT CCT	3395
GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
TTG AGA GAG	GGA GAA GAG	TGA			3542
GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	TGTGATATGA	3642
GGCCCATTC	TGCCTCTTTG	AAGAGAGCAG	TCAGCATTCT	TAGCAGTGAG	3692
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
TTGTTCAAAT	GTTCCTTTTA	ACAAATGGTT	GGATGAACTT	CAGCATCCAA	3792
GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
TAAGAGTCCT	GTTTTTTTATT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892
TTGTCACATA	ATAACAGCAG	TGGAATATGT	ATTTGCCTAT	ATTGTGAACG	3942
AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
TGCCTTATAC	CTCAGTCTAT	TATGTAAAAT	TAAAAATATG	TGTATGTTTT	4042
TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
TCACTGGCTC	ATTTCTTTAC	CATTCACTCA	GCATCTGCTC	TGTGGAAGGC	4142
CCTGGTAGTA	GTGGG				4157

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG	AAGCCGGCCC	AGGCTCGGTG	AGGAGGCAAG	GTTCTGAGGG	50
GACAGGCTGA	CCTGGAGGAC	CAGAGGCCCC	CGGAGGAGCA	CTGAAGGAGA	100
AGATCTGCCA	GTGGGTCTCC	ATTGCCCAGC	TCCTGCCAC	ACTCCCGCCT	150
GTTGCCCTGA	CCAGAGTCAT	C			171
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG	CCT GAA GAA	213
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG	GTG GGT GCG	255
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCC TCT	297
TCT ACT CTA	GTT GAA GTC	ACC CTG GGG	GAG GTG	CCT GCT GCC	339
GAG TCA CCA	GAT CCT CCC	CAG AGT CCT	CAG GGA GCC	TCC AGC	381
CTC CCC ACT	ACC ATG AAC	TAC CCT CTC	TGG AGC CAA	TCC TAT	423
GAG GAC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGC	ACC TTC	465
CCT GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA CTC AGT	AGG AAG	507

GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC	549
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC	591
GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT	633
TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA	675
GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG	717
GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG	759
CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA	801
AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG	843
CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG	885
TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG	927
GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT	969
GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA	1011
ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT	1053
GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT	1095
TTG AGA GAG GGG GAA GAG TGA	1116
GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT	1166
GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA	1216
GGCCCATTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG	1266
TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG	1316
TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG	1366
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG	1416
TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA	1466
TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC	1516
GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG	1566
ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA	1616
ACCAGGATTT CCTTGACTTC TTTG	1640

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-31 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT	50
CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG	100
GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG	150
AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA	200
GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC	250
CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT	300
TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC	350
CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC	400
AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG	450
TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC	500
TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCTGCCACA	550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580

ATG	CCT	CTT	GAG	CAG	AGG	AGT	CAG	CAC	TGC	AAG	CCT	GAA	GAA	622
GGC	CTT	GAG	GCC	CGA	GGA	GAG	GCC	CTG	GGC	CTG	GTG	GGT	GCG	664
CAG	GCT	CCT	GCT	ACT	GAG	GAG	CAG	GAG	GCT	GCC	TCC	TCC	TCT	706
TCT	AGT	GTA	GTT	GAA	GTC	ACC	CTG	GGG	GAG	GTG	CCT	GCT	GCC	748
GAG	TCA	CCA	GAT	CCT	CCC	CAG	AGT	CCT	CAG	GGA	GCC	TCC	AGC	790
CTC	CCC	ACT	ACC	ATG	AAC	TAC	CCT	CTC	TGG	AGC	CAA	TCC	TAT	832
GAG	GAC	TCC	AGC	AAC	CAA	GAA	GAG	GAG	GGG	CCA	AGC	ACC	TTC	874
CCT	GAC	CTG	GAG	TCT	GAG	TTC	CAA	GCA	GCA	CTC	AGT	AGG	AAG	916
GTG	GCC	AAG	TTG	GTT	CAT	TTT	CTG	CTC						943

(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-4 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCAGGC	CCTGCCTGGA	GAAATGTGAG	GGCCCTGAGT	GAACACAGTG	50									
GGGATCATCC	ACTCCATGAG	AGTGGGGACC	TCACAGAGTC	CAGCCTACCC	100									
TCTTGATGGC	ACTGAGGGAC	CGGGGCTGTG	CTTACAGTCT	GCACCCTAAG	150									
GGCCCATGGA	TTCCTCTCCT	AGGAGCTCCA	GGAACAAGGC	AGTGAGGCCT	200									
TGGTCTGAGA	CAGTGTCTCT	AGGTTACAGA	GCAGAGGATG	CACAGGCTGT	250									
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300									
CAAGACACAT	AGGACTCCAA	AGAGTCTGGC	CTCACCTCCC	TACCATCAAT	350									
CCTGCAGAAT	CGACCTCTGC	TGGCCGGCTA	TACCCTGAGG	TGCTCTCTCA	400									
CTTCCTCCTT	CAGGTTCTGA	GCAGACAGGC	CAACCGGAGA	CAGGATTCCC	450									
TGGAGGCCAC	AGAGGAGCAC	CAAGGAGAAG	ATCTGTAAGT	AAGCCTTTGT	500									
TAGAGCCTCT	AAGATTTGGT	TCTCAGCTGA	GGTCTCTCAC	ATGCTCCCTC	550									
TCTCCGTAGG	CCTGTGGGTC	CCCATTGCCC	AGCTTTTGCC	TGCACTCTTG	600									
CCTGCTGCCC	TGACCAGAGT	CATC			624									
ATG	TCT	TCT	GAG	CAG	AAG	AGT	CAG	CAC	TGC	AAG	CCT	GAG	GAA	666
GGC	GTT	GAG	GCC	CAA	GAA	GAG	GCC	CTG	GGC	CTG	GTG	GGT	GCA	708
CAG	GCT	CCT	ACT	ACT	GAG	GAG	CAG	GAG	GCT	GCT	GTC	TCC	TCC	750
TCC	TCT	CCT	CTG	GTC	CCT	GGC	ACC	CTG	GAG	GAA	GTG	CCT	GCT	792
GCT	GAG	TCA	GCA	GGT	CCT	CCC	CAG	AGT	CCT	CAG	GGA	GCC	TCT	834
GCC	TTA	CCC	ACT	ACC	ATC	AGC	TTC	ACT	TGC	TGG	AGG	CAA	CCC	876
AAT	GAG	GGT	TCC	AGC	AGC	CAA	GAA	GAG	GAG	GGG	CCA	AGC	ACC	918
TCG	CCT	GAC	GCA	GAG	TCC	TTG	TTC	CGA	GAA	GCA	CTC	AGT	AAC	960
AAG	GTG	GAT	GAG	TTG	GCT	CAT	TTT	CTG	CTC	CGC	AAG	TAT	CGA	1002
GCC	AAG	GAG	CTG	GTC	ACA	AAG	GCA	GAA	ATG	CTG	GAG	AGA	GTC	1044
ATC	AAA	AAT	TAC	AAG	CGC	TGC	TTT	CCT	GTG	ATC	TTC	GGC	AAA	1086
GCC	TCC	GAG	TCC	CTG	AAG	ATG	ATC	TTT	GGC	ATT	GAC	GTG	AAG	1128
GAA	GTG	GAC	CCC	GCC	AGC	AAC	ACC	TAC	ACC	CTT	GTC	ACC	TGC	1170
CTG	GGC	CTT	TCC	TAT	GAT	GGC	CTG	CTG	GGT	AAT	AAT	CAG	ATC	1212
TTT	CCC	AAG	ACA	GGC	CTT	CTG	ATA	ATC	GTC	CTG	GGC	ACA	ATT	1254
GCA	ATG	GAG	GGC	GAC	AGC	GCC	TCT	GAG	GAG	GAA	ATC	TGG	GAG	1296

00019669-031797

GAG CTG GGT GTG ATG GGG GTG TAT GAT GGG AGG GAG CAC ACT	1338
GTC TAT GGG GAG CCC AGG AAA CTG CTC ACC CAA GAT TGG GTG	1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG GTA CCC GGC AGT AAT	1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT CCA AGG GCT CTG GCT	1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG CAT GTG GTC AGG GTC	1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA TCC CTG CGT GAA GCA	1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC TGA	1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGGCAGGGCT GGGCCAGTGC	1628
ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCCTCGTGTA ACATGAGGCC	1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGTGTTCTTA GTAGTGGGTT	1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTCTGTTTCC TTTTACAATT	1778
GTTGAAATGT TCCTTTTAAT GGATGGTTGA ATTAACCTCA GCATCCAAGT	1828
TTATGAATCG TAGTTAACGT ATATTGCTGT TAATATAGTT TAGGAGTAAG	1878
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGTTCTATTT TGTGAATTTG	1928
GGACATAATA ACAGCAGTGG AGTAAGTATT TAGAAGTGTG AATTCACCGT	1978
GAAATAGGTG AGATAAATTA AAAGATACTT AATTCCTGCC TTATGCCTCA	2028
GTCTATTCTG TAAAATTTAA AAATATATAT GCATACCTGG ATTTCTTGG	2078
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATAAATAATT CTTTCTGTTA	2128
ACTGGCTCAT TTCTTCTCTA TGCAGTGGC ATCTGCTCTG TGAAGGCCCC	2178
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAGACACACA CCTACCGATA	2228
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAATTAAGGT GACAAGATGT	2278
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTGGGTATGG GGCTCCAGGT	2328
GAGAGTGGTC GGGTGTAAT TCCCTGTGTG GGGCCTTTTG GGCTTTGGGA	2378
AACTGCATTT TCTTCTGAGG GATCTGATTC TAATGAAGCT TGGTGGGTCC	2428
AGGGCCAGAT TCTCAGAGGG AGAGGGGAAA GCCCAGATTG GAAAAGTTGC	2478
TCTGAGCAGT TCCTTTGTGA CAATGGATGA ACAGAGAGGA GCCTCTACCT	2528
GGG	2531

(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2531 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-41 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG	150
GGCCCATGGA TTCCTCTCCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
TGGTCTGAGA CAGTGTCTCT AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA	400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550

TCTCCGTAGG	CCTGTGGGTC	CCCATTGCCC	AGCTTTTGCC	TGCACTCTTG	600
CCTGCTGCCC	TGAGCAGAGT	CATC			624
ATG TCT TCT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	666
GGC GTT GAG	GCC CAA GAA	GAG GCC CTG	GGC CTG GTG	GGT GCG	708
CAG GCT CCT	ACT ACT GAG	GAG CAG GAG	GCT GCT GTC	TCC TCC	750
TCC TCT CCT	CTG GTC CCT	GGC ACC CTG	GAG GAA GTG	CCT GCT	792
GCT GAG TCA	GCA GGT CCT	CCC CAG AGT	CCT CAG GGA	GCC TCT	834
GCC TTA CCC	ACT ACC ATC	AGC TTC ACT	TGC TGG AGG	CAA CCC	876
AAT GAG GGT	TCC AGC AGC	CAA GAA GAG	GAG GAG GGG	CCA AGC	918
TCG CCT GAC	GCA GAG TCC	TTG TTC CGA	GAA GCA CTC	AGT AAC	960
AAG GTG GAT	GAG TTG GCT	CAT TTT CTG	CTC CGC AAG	TAT CGA	1002
GCC AAG GAG	CTG GTC ACA	AAG GCA GAA	ATG CTG GAG	AGA GTC	1044
ATC AAA AAT	TAC AAG CGC	TGC TTT CCT	GTG ATC TTC	GGC AAA	1086
GCC TCC GAG	TCC CTG AAG	ATG ATC TTT	GGC ATT GAC	GTG AAG	1128
GAA GTG GAC	CCC ACC AGC	AAC ACC TAC	ACC CTT GTC	ACC TGC	1170
CTG GGC CTT	TCC TAT GAT	GGC CTG CTG	GGT AAT AAT	CAG ATC	1212
TTT CCC AAG	ACA GGC CTT	CTG ATA ATC	GTC CTG GGC	ACA ATT	1254
GCA ATG GAG	GGC GAC AGC	GCC TCT GAG	GAG GAG GAA	ATC TGG	1296
GAG CTG GGT	GTG ATG GGG	GTG TAT GAT	GGG AGG GAG	CAC ACT	1338
GTC TAT GGG	GAG CCC AGG	AAA CTG CTC	ACC CAA GAT	TGG GTG	1380
CAG GAA AAC	TAC CTG GAG	TAC CGG CAG	GTA CCC GGC	AGT AAT	1422
CCT GCG CGC	TAT GAG TTC	CTG TGG GGT	CCA AGG GCT	CTG GCT	1464
GAA ACC AGC	TAT GTG AAA	GTC CTG GAG	CAT GTG GTC	AGG GTC	1506
AAT GCA AGA	GTT CGC ATT	GCC TAC CCA	TCC CTG CGT	GAA GCA	1548
GCT TTG TTA	GAG GAG GAA	GAG GGA GTC	TGA		1578
GCATGAGTTG	CAGCCAGGGC	TGTGGGGAAG	GGGCAGGGCT	GGGCCAGTGC	1628
ATCTAACAGC	CCTGTGCAGC	AGCTTCCCTT	GCCTCGTGTA	ACATGAGGCC	1678
CATTCTTCAC	TCTGTTTGAA	GAAAATAGTC	AGTGTCTTA	GTAGTGGGTT	1728
TCTATTTTGT	TGGATGACTT	GGAGATTTAT	CTCTGTTTCC	TTTTACAATT	1778
GTTGAAATGT	TCCTTTTAAT	GGATGGTTGA	ATTAACTTCA	GCATCCAAGT	1828
TTATGAATCG	TAGTTAACGT	ATATTGCTGT	TAATATAGTT	TAGGAGTAAG	1878
AGTCTTGTTT	TTTATTCAGA	TTGGGAAATC	CGTTCTATTT	TGTGAATTTG	1928
GGACATAATA	ACAGCAGTGG	AGTAAGTATT	TAGAAGTGTG	AATTCACCGT	1978
GAAATAGGTG	AGATAAATTA	AAAGATACTT	AATTCCCGCC	TTATGCCTCA	2028
GTCTATTCTG	TAAAATTTAA	AAATATATAT	GCATACCTGG	ATTTCTTGG	2078
CTTCGTGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAATAATT	CTTTCTGTTA	2128
ACTGGCTCAT	TTCTTCTCTA	TGCACTGAGC	ATCTGCTCTG	TGGAAGGCCC	2178
AGGATTAGTA	GTGGAGATAC	TAGGGTAAGC	CAGACACACA	CCTACCGATA	2228
GGGTATTAAG	AGTCTAGGAG	CGCGGTCATA	TAATTAAGGT	GACAAGATGT	2278
CCTCTAAGAT	GTAGGGGAAA	AGTAACGAGT	GTGGGTATGG	GGCTCCAGGT	2328
GAGAGTGGTC	GGGTGTAAAT	TCCCTGTGTG	GGGCCTTTTG	GGCTTTGGGA	2378
AACTCCATTT	TCTTCTGAGG	GATCTGATTC	TAATGAAGCT	TGGTGGGTCC	2428
AGGGCCAGAT	TCTCAGAGGG	AGAGGGAAAA	GCCCAGATTG	GAAAAGTTGC	2478
TCTGAGCGGT	TCCTTTGTGA	CAATGGATGA	ACAGAGAGGA	GCCTCTACCT	2528
GGG					2531

- (2) INFORMATION FOR SEQUENCE ID NO: 15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1068 bas pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA to mRNA
 - (ix) FEATURE:
 - (A) NAME/KEY: cDNA MAGE-4
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

03819669-031797

G GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	40
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	82
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	124
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	166
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	208
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	250
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	292
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	334
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	376
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	418
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	460
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	502
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	544
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	586
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	628
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	670
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG	720
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	770
GCCCATCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG	820
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	870
ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTA ACT TCAGCATCCA	920
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	970
AAGAGTCTTG TTTTATTATC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT	1020
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1068

- (2) INFORMATION FOR SEQUENCE ID NO: 16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2226 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-5 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT GAGCACAGAG	50
GGGACCATTG ACCCAAGAG GGTGGAGACC TCACAGATTG CAGCCTACCC	100

TCCTGTTAGC	ACTGGGGGCC	TGAGGCTGTG	CTTGCACTCT	GCACCCTGAG	150
GGCCCATGCA	TTCCTCTTCC	AGGAGCTCCA	GGAAACAGAC	ACTGAGGCCT	200
TGGTCTGAGG	CCGTGCCCTC	AGGTCACAGA	GCAGAGGAGA	TGCAGACGTC	250
TAGTGCCAGC	AGTGAACGTT	TGCCTTGAAT	GCACACTAAT	GGCCCCCATC	300
GCCCCAGAAC	ATATGGGACT	CCAGAGCACC	TGGCCTCACC	CTCTCTACTG	350
TCAGTCCTGC	AGAATCAGCC	TCTGCTTGCT	TGTGTACCCCT	GAGGTGCCCT	400
CTCACTTTTT	CCTTCAGGTT	CTCAGGGGAC	AGGCTGACCA	GGATCACCAG	450
GAAGCTCCAG	AGGATCCCCA	GGAGGCCCTA	GAGGAGCACC	AAAGGAGAAG	500
ATCTGTAAGT	AAGCCTTTGT	TAGAGCCTCC	AAGGTTCACT	TTTGTAGCTGA	550
GGCTTCTCAC	ATGCTCCCTC	TCTCTCCAGG	CCAGTGGGTC	TCCATTGCCC	600
AGCTCCTGCC	CACACTCCTG	CCTGTTGCGG	TGACCAGAGT	CGTC	644
ATG TCT CTT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	686
CTC CTC TGG	TCC CAG GCA	CCC TGG GGG	AGG TGC CTG	CTG CTG	728
GGT CAC CAG	GTC CTC TCA	AGA GTC CTC	AGG GAG CCT	CCG CCA	770
TCC CCA CTG	CCA TCG ATT	TCA CTC TAT	GGA GGC AAT	CCA TTA	812
AGG GCT CCA	GCA ACC AAG	AAG AGG AGG	GGC CAA GCA	CCT CCC	854
CTG ACC CAG	AGT CTG TGT	TCC GAG CAG	CAC TCA GTA	AGA AGG	896
TGG CTG ACT	TGA				908
TTCATTTTCT	GCTCCTCAAG	TATTAAGTCA	AGGAGCTGGT	CACAAAGGCA	958
GAAATGCTGG	AGAGCGTCAT	CAAAAATTAC	AAGCGCTGCT	TTCCTGAGAT	1008
CTTCGGCAAA	GCCTCCGAGT	CCTTGCAGCT	GGTCTTTGGC	ATTGACGTGA	1058
AGGAAGCGGA	CCCCACCAGC	AACACCTACA	CCCTTGTCAC	CTGCCTGGGA	1108
CTCCTATGAT	GGCCTGCTGG	TTGATAATAA	TCAGATCATG	CCCAAGACGG	1158
GCCTCCTGAT	AATCGTCTTG	GGCATGATTG	CAATGGAGGG	CAAATGCGTC	1208
CCTGAGGAGA	AAATCTGGGA	GGAGCTGAGT	GTGATGAAGG	TGTATGTTGG	1258
GAGGGAGCAC	AGTGTCTGTG	GGGAGCCCAG	GAAGCTGCTC	ACCCAAGATT	1308
TGGTGCAGGA	AAACTACCTG	GAGTACCGGC	AGGTGCCCCAG	CAGTGATCCC	1358
ATATGCTATG	AGTTACTGTG	GGGTCCAAGG	GCACTCGCTG	CTTGAAAGTA	1408
CTGGAGCACG	TGGTCAGGGT	CAATGCAAGA	GTTCTCATTT	CCTACCCATC	1458
CCTGCGTGAA	GCAGCTTTGA	GAGAGGAGGA	AGAGGGAGTC	TGAGCATGAG	1508
CTGCAGCCAG	GGCCACTGCG	AGGGGGGCTG	GGCCAGTGCA	CCTTCCAGGG	1558
CTCCGTCCAG	TAGTTTCCCC	TGCCTTAATG	TGACATGAGG	CCCATTCTTC	1608
TCTCTTTGAA	GAGAGCAGTC	AACATTCTTA	GTAGTGGGTT	TCTGTTCTAT	1658
TGGATGACTT	TGAGATTTGT	CTTTGTTTCC	TTTTGGAATT	GTTCAAATGT	1708
TTCTTTTAAT	GGGTGGTTGA	ATGAACTTCA	GCATTCAAAT	TTATGAATGA	1758
CAGTAGTCAC	ACATAGTGCT	GTTTATATAG	TTTAGGAGTA	AGAGTCTTGT	1808
TTTTTTATTCA	GATTGGGAAA	TCCATTCCAT	TTTGTGAATT	GGGACATAGT	1858
TACAGCAGTG	GAATAAGTAT	TCATTTAGAA	ATGTGAATGA	GCAGTAAAAC	1908
TGATGACATA	AAGAAATTAA	AAGATATTTA	ATTCTTGCTT	ATACTCAGTC	1958
TATTCGGTAA	AATTTTTTTT	AAAAAATGTG	CATACCTGGA	TTTCCTTGGC	2008
TTCTTTGAGA	ATGTAAGACA	AATTAAATCT	GAATAAATCA	TTCTCCCTGT	2058
TCACCTGGCTC	ATTTATTCTC	TATGCACTGA	GCATTTGCTC	TGTGGAAGGC	2108
CCTGGGTAA	TAGTGGAGAT	GCTAAGGTAA	GCCAGACTCA	CCCCTACCCA	2158
CAGGGTAGTA	AAGTCTAGGA	GCAGCAGTCA	TATAATTAAG	GTGGAGAGAT	2208
GCCCTCTAAG	ATGTAGAG				2226

- (2) INFORMATION FOR SEQUENCE ID NO: 17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-51 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

GGATCCAGGC	CTTGCCAGGA	GAAAGGTGAG	GGCCCTGTGT	GAGCACAGAG	50
GGGACCATTC	ACCCCAAGAG	GGTGGAGACC	TCACAGATTC	CAGCCTACCC	100
TCCTGTTAGC	ACTGGGGGCC	TGAGGCTGTG	CTTGCACTCT	GCACCCTGAG	150
GGCCCATGCA	TTCCTCTTCC	AGGAGCTCCA	GGAAACAGAC	ACTGAGGCCT	200
TGGTCTGAGG	CCGTGCCCTC	AGGTCACAGA	GCAGAGGAGA	TGCAGACGTC	250
TAGTGCCAGC	AGTGAACGTT	TGCCTTGAAT	GCACACTAAT	GGCCCCCATC	300
GCCCCAGAAC	ATATGGGACT	CCAGAGCACC	TGGCCTCACC	CTCTCTACTG	350
TCAGTCCTGC	AGAATCAGCC	TCTGCTTGCT	TGTGTACCCCT	GAGGTGCCCT	400
CTCACTTTTT	CCTTCAGGTT	CTCAGGGGAC	AGGCTGACCA	GGATCACCAG	450
GAAGCTCCAG	AGGATCCCCA	GGAGGCCCTA	GAGGAGCACC	AAAGGAGAAG	500
ATCTGTAAAGT	AAGCCTTTGT	TAGAGCCTCC	AAGGTTCACT	TTTGTAGCTGA	550
GGCTTCTCAC	ATGCTCCCTC	TCTCTCCAGG	CCAGTGGGTC	TCCATTGCCC	600
AGCTCCTGCC	CACACTCCTG	CCTGTTGCGG	TGACCAGAGT	CGTC	644
ATG TCT CTT	GAG CAG AAG	AGT CAG CAC	TGC AAG CCT	GAG GAA	686
GGC CTT GAC	ACC CAA GAA	GAG CCC TGG	GCC TGG TGG	GTG TGC	728
AGG CTG CCA	CTA CTG AGG	AGC AGG AGG	CTG TGT CCT	CCT CCT	770
CTC CTC TGG	TCC CAG GCA	CCC TGG GGG	AGG TGC CTG	CTG CTG	812
GGT CAC CAG	GTC CTC TCA	AGA GTC CTC	AGG GAG CCT	CCG CCA	854
TCC CCA CTG	CCA TCG ATT	TCA CTC TAT	GGA GGC AAT	CCA TTA	896
AGG GCT CCA	GCA ACC AAG	AAG AGG AGG	GGC CAA GCA	CCT CCC	938
CTG ACC CAG	AGT CTG TGT	TCC GAG CAG	CAC TCA GTA	AGA AGG	980
TGG CTG ACT	TGA				992
TTCATTTTCT	GCTCCTCAAG	TATTAAGTCA	AGGAGCCGGT	CACAAAGGCA	1042
GAAATGCTGG	AGAGCGTCAT	CAAAAATTAC	AAGCGCTGCT	TTCCTGAGAT	1092
CTTCGGCAAA	GCCTCCGAGT	CCTTGCAGCT	GGTCTTTGGC	ATTGACGTGA	1142
AGGAAGCGGA	CCCCACCAGC	AACACCTACA	CCCTTGTCAC	CTGCCTGGGA	1192
CTCCTATGAT	GGCCTGGTGG	TTTAATCAGA	TCATGCCCAA	GACGGGCCTC	1242
CTGATAATCG	TCTTGGGCAT	GATTGCAATG	GAGGGCAAAT	GCGTCCCTGA	1292
GGAGAAAATC	TGGGAGGAGC	TGGGTGTGAT	GAAGGTGTAT	GTTGGGAGGG	1342
AGCACAGTGT	CTGTGGGGAG	CCCAGGAAGC	TGCTCACCCA	AGATTTGGTG	1392
CAGGAAAAC	ACCTGGAGTA	CCGCAGGTGC	CCAGCAGTGA	TCCCATATGC	1442
TATGAGTTAC	TGTGGGGTCC	AAGGGCACTC	GCTGCTTGAA	AGTACTGGAG	1492
CACGTGGTCA	GGGTCAATGC	AAGAGTTCTC	ATTTCTTACC	CATCCCTGCA	1542
TGAAGCAGCT	TTGAGAGAGG	AGGAAGAGGG	AGTCTGAGCA	TGAGCTGCAG	1592
CCAGGGCCAC	TGCGAGGGGG	GCTGGGCCAG	TGCACCTTCC	AGGGCTCCGT	1642
CCAGTAGTTT	CCCCTGCCTT	AATGTGACAT	GAGGCCCATT	CTTCTCTCTT	1692
TGAAGAGAGC	AGTCAACATT	CTTAGTAGTG	GGTTTCTGTT	CTATTGGATG	1742
ACTTTGAGAT	TTGTCTTTGT	TTCCTTTTGG	AATTGTTCAA	ATGTTCTTTT	1792
TAATGGGTGG	TTGAATGAAC	TTCAGCATTC	AAATTTATGA	ATGACAGTAG	1842
TCACACATAG	TGCTGTTTAT	ATAGTTTAGG	AGTAAGAGTC	TTGTTTTTTA	1892
TTCAGATTGG	GAAATCCATT	CCATTTTGTG	AATTGGGACA	TAGTTACAGC	1942

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AGTGG AATAA	GTATTCATTT	AGAAATGTGA	ATGAGCAGTA	AAACTGATGA	1992
GATAAAGAAA	TTAAAAGATA	TTTAATTCTT	GCCTTATACT	CAGTCTATTC	2042
GGTAAAATTT	TTTTTTAAAA	ATGTGCATAC	CTGGATTTC	TTGGCTTCTT	2092
TGAGAATGTA	AGACAAATTA	AATCTGAATA	AATCATTCTC	CCTGTTCACT	2142
GGCTCATTTA	TTCTCTATGC	ACTGAGCATT	TGCTCTGTGG	AAGGCCCTGG	2192
GTTAATAGTG	GAGATGCTAA	GGTAAGCCAG	ACTCACCCCT	ACCCACAGGG	2242
TAGTAAAGTC	TAGGAGCAGC	AGTCATATAA	TTAAGGTGGA	GAGATGCCCT	2292
CTAAGATGTA	GAG				2305

(2) INFORMATION FOR SEQUENCE ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-6 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	TCC	GAT	TCC	TTG	42
CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	GTG	GAC	CCC	ATC	84
GGC	CAC	GTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	GGC	CTC	TCC	TAC	126
GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	CCC	AGG	ACA	GGC	168
TTC	CTG	ATA	ATC	ATC	CTG	GCC	ATA	ATC	GCA	AGA	GAG	GGC	GAC	210
TGT	GCC	CCT	GAG	GAG										225

(2) INFORMATION FOR SEQUENCE ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1947 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-7 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA	ACAAGGGCCC	CACACTCCCC	AGAACACAAG	GGA CTCCAGA	50
GAGCC CAGCC	TCACCTTCCC	TACTGT CAGT	CCTGCAGCCT	CAGCCTCTGC	100
TGGCCGGCTG	TACCCTGAGG	TGCCCTCTCA	CTTCCTCCTT	CAGGTTCTCA	150
GCGGACAGGC	CGGCCAGGAG	GTCAGAAGCC	CCAGGAGGCC	CCAGAGGAGC	200
ACCGAAGGAG	AAGATCTGTA	AGTAGGCCTT	TGTTAGGGCC	TCCAGGGCGT	250
GGTTCACAAA	TGAGGCCCTT	CACAAGCTCC	TTCTCTCCCC	AGATCTGTGG	300
GTTCCTCCCC	ATCGCCCAGC	TGCTGCCCGC	ACTCCAGCCT	GCTGCCCTGA	350
CCAGAGTCAT	CATGTCTTCT	GAGCAGAGGA	GTCAGCACTG	CAAGCCTGAG	400

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GATGCCTTGA	GGCCCAAGGA	CAGGAGGCTC	TGGGCCTGGT	GGGTGCGCAG	450
GCTCCCGCCA	CCGAGGAGCA	CGAGGCTGCC	TCCTCCTTCA	CTCTGATTGA	500
AGGCACCCTG	GAGGAGGTGC	CTGCTGCTGG	GTCCCCCAGT	CCTCCCCTGA	550
GTCTCAGGGT	TCCTCCTTTT	CCCTGACCAT	CAGCAACAAC	ACTCTATGGA	600
GCCAATCCAG	TGAGGGCACC	AGCAGCCGGG	AAGAGGAGGG	GCCAACCACC	650
TAGACACACC	CCGCTCACCT	GGCGTCCTTG	TTCCA		685
ATG GGA AGG	TGG CTG AGT	TGG TTC GCT	TCC TGC TGC	ACA AGT	727
ATC GAG TCA	AGG AGC TGG	TCA CAA AGG	CAG AAA TGC	TGG ACA	769
GTG TCA TCA	AAA ATT ACA	AGC ACT AGT	TTC CTT GTG	ATC TAT	811
GGC AAA GCC	TCA GAG TGC	ATG CAG GTG	ATG TTT GGC	ATT GAC	853
ATG AAG GAA	GTG GAC CCC	GCG GCC ACT	CCT ACG TCC	TTG TCA	895
CCT GCT TGG	GCC TCT CCT	ACA ATG GCC	TGC TGG GTG	ATG ATC	937
AGA GCA TGC	CCG AGA CCG	GCC TTC TGA			964
TTATGGTCTT	GACCATGATC	TTAATGGAGG	GCCACTGTGC	CCCTGAGGAG	1014
GCAATCTGGG	AAGCGTTGAG	TGTAATGGTG	TATGATGGGA	TGGAGCAGTT	1064
TCTTTGGGCA	GCTGAGGAAG	CTGCTCACCC	AAGATTGGGT	GCAGGAAAAC	1114
TACCTGCAAT	ACCGCCAGGT	GCCCAGCAGT	GATCCCCCGT	GCTACCAGTT	1164
CCTGTGGGGT	CCAAGGGCCC	TCATTGAAAC	CAGCTATGTG	AAAGTCCTGG	1214
AGTATGCAGC	CAGGGTCAGT	ACTAAAGAGA	GCATTTCCCTA	CCCATCCCTG	1264
CATGAAGAGG	CTTTGGGAGA	GGAGGAAGAG	GGAGTCTGAG	CAGAAGTTGC	1314
AGCCAGGGCC	AGTGGGGCAG	ATTGGGGGAG	GGCCTGGGCA	GTGCACGTTC	1364
CACACATCCA	CCACCTTCCC	TGTCCTGTTA	CATGAGGCCC	ATTCTTCACT	1414
CTGTGTTTGA	AGAGAGCAGT	CAATGTTCTC	AGTAGCGGGG	AGTGTGTTGG	1464
GTGTGAGGGA	ATACAAGGTG	GACCATCTCT	CAGTTCCTGT	TCTCTTGGGC	1514
GATTTGGAGG	TTTATCTTTG	TTTCCTTTTG	CAGTCGTTCA	AATGTTCTTT	1564
TTAATGGATG	GTGTAATGAA	CTTCAACATT	CATTTTCATGT	ATGACAGTAG	1614
GCAGACTTAC	TGTTTTTTTAT	ATAGTTAAAA	GTAAGTGCAT	TGTTTTTTTAT	1664
TTATGTAAGA	AAATCTATGT	TATTTCTTGA	ATTGGGACAA	CATAACATAG	1714
CAGAGGATTA	AGTACCTTTT	ATAATGTGAA	AGAACAAAGC	GGTAAAATGG	1764
GTGAGATAAA	GAAATAAAGA	AATTAAATTG	GCTGGGCACG	GTGGCTCACG	1814
CCTGTAATCC	CAGCACTTTA	GGAGGCAGAG	GCACGGGGAT	CACGAGGTCA	1864
GGAGATCGAG	ACCATTCTGG	CTAACACAGT	GAAACACCAT	CTCTATTAAA	1914
AATACAAAAC	TTAGCCGGGC	GTGGTGGCGG	GTG		1947

(2) INFORMATION FOR SEQUENCE ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1810 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGE-8 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

GAGCTCCAGG	AACCAGGCTG	TGAGGTCTTG	GTCTGAGGCA	GTATCTTCAA	50
TCACAGAGCA	TAAGAGGCCC	AGGCAGTAGT	AGCAGTCAAG	CTGAGGTGGT	100
GTTTCCCCTG	TATGTATACC	AGAGGCCCTT	CTGGCATCAG	AACAGCAGGA	150
ACCCACAGT	TCCTGGCCCT	ACCAGCCCTT	TTGTCAGTCC	TGGAGCCTTG	200
GCCTTTGCCA	GGAGGCTGCA	CCCTGAGATG	CCCTCTCAAT	TTCTCCTTCA	250
GGTTCGCAGA	GAACAGGCCA	GCCAGGAGGT	CAGGAGGCCC	CAGAGAAGCA	300

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CTGAAGAAGA CCTGTAAGTA GACCTTTGTT AGGGCATCCA GGGTGTAGTA	350
CCCAGCTGAG GCCTCTCACA CGCTTCCTCT CTCCCCAGGC CTGTGGGTCT	400
CAATTGCCCC GCTCCGGCCC AACTCTCCT GCTGCCCTGA CCTGAGTCAT	450
C	451
ATG CTT CTT GGG CAG AAG AGT CAG CGC TAC AAG GCT GAG GAA	493
GGC CTT CAG GCC CAA GGA GAG GCA CCA GGG CTT ATG GAT GTG	535
CAG ATT CCC ACA GCT GAG GAG CAG AAG GCT GCA TCC TCC TCC	577
TCT ACT CTG ATC ATG GGA ACC CTT GAG GAG GTG ACT GAT TCT	619
GGG TCA CCA AGT CCT CCC CAG AGT CCT GAG GGT GCC TCC TCT	661
TCC CTG ACT GTC ACC GAC AGC ACT CTG TGG AGC CAA TCC GAT	703
GAG GGT TCC AGC AGC AAT GAA GAG GAG GGG CCA AGC ACC TCC	745
CCG GAC CCA GCT CAC CTG GAG TCC CTG TTC CGG GAA GCA CTT	787
GAT GAG AAA GTG GCT GAG TTA GTT CGT TTC CTG CTC CGC AAA	829
TAT CAA ATT AAG GAG CCG GTC ACA AAG GCA GAA ATG CTT GAG	871
AGT GTC ATC AAA AAT TAC AAG AAC CAC TTT CCT GAT ATC TTC	913
AGC AAA GCC TCT GAG TGC ATG CAG GTG ATC TTT GGC ATT GAT	955
GTG AAG GAA GTG GAC CCT GCC GGC CAC TCC TAC ATC CTT GTC	997
ACC TGC CTG GGC CTC TCC TAT GAT GGC CTG CTG GGT GAT GAT	1039
CAG AGT ACG CCC AAG ACC GGC CTC CTG ATA ATC GTC CTG GGC	1081
ATG ATC TTA ATG GAG GGC AGC CGC GCC CCG GAG GAG GCA ATC	1123
TGG GAA GCA TTG AGT GTG ATG GGG GCT GTA TGA	1156
TGGGAGGGAG CACAGTGTCT ATTGGAAGCT CAGGAAGCTG CTCACCCAAG	1206
AGTGGGTGCA GGAGAACTAC CTGGAGTACC GCCAGGCGCC CGGCAGTGAT	1256
CCTGTGCGCT ACGAGTTCCT GTGGGGTCCA AGGGCCCTTG CTGAAACCAG	1306
CTATGTGAAA GTCCTGGAGC ATGTGGTCAG GGTCAATGCA AGAGTTCGCA	1356
TTTCCTACCC ATCCCTGCAT GAAGAGGCTT TGGGAGAGGA GAAAGGAGTT	1406
TGAGCAGGAG TTGCAGCTAG GGCCAGTGGG GCAGGTTGTG GGAGGGCCTG	1456
GGCCAGTGCA CGTTCCAGGG CCACATCCAC CACTTTCCT GCTCTGTTAC	1506
ATGAGGCCCA TTCTTCACTC TGTGTTTGAA GAGAGCAGTC ACAGTTCTCA	1556
GTAGTGGGGA GCATGTTGGG TGTGAGGGAA CACAGTGTGG ACCATCTCTC	1606
AGTTCCTGTT CTATTGGGCG ATTTGGAGGT TTATCTTTGT TTCCTTTTGG	1656
AATTGTTCCA ATGTTCTTTC TAATGGATGG TGTAATGAAC TTCAACATTC	1706
ATTTTATGTA TGACAGTAGA CAGACTTACT GCTTTTATA TAGTTTAGGA	1756
GTAAGAGTCT TGCTTTTCAT TTATACTGGG AAACCCATGT TATTTCTTGA	1806
ATTC	1810

(2) INFORMATION FOR SEQUENCE ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-9 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

TCTGAGACAG TGCCTCAGG TCGCAGAGCA GAGGAGACCC AGGCAGTGTC	50
AGCAGTGAAG GTGAAGTGTT CACCCTGAAT GTGCACCAAG GGCCCCACCT	100
GCCCCAGCAC ACATGGGACC CCATAGCACC TGGCCCCATT CCCCCTACTG	150
TCACTCATAG AGCCTTGATC TCTGCAGGCT AGCTGCACGC TGAGTAGCCC	200

TCTCACTTCC	TCCCTCAGGT	TCTCGGGACA	GGCTAACCAG	GAGGACAGGA	250
GCCCCAAGAG	GCCCCAGAGC	AGCACTGACG	AAGACCTGTA	AGTCAGCCTT	300
TGTTAGAACC	TCCAAGGTTT	GGTTCTCAGC	TGAAGTCTCT	CACACACTCC	350
CTCTCTCCCC	AGGCCTGTGG	GTCTCCATCG	CCCAGCTCCT	GCCCACGCTC	400
CTGACTGCTG	CCCTGACCAG	AGTCATC			427
ATG TCT CTC	GAG CAG AGG	AGT CCG CAC	TGC AAG CCT	GAT GAA	469
GAC CTT GAA	GCC CAA GGA	GAG GAC TTG	GGC CTG ATG	GGT GCA	511
CAG GAA CCC	ACA GGC GAG	GAG GAG GAG	ACT ACC TCC	TCC TCT	553
GAC AGC AAG	GAG GAG GTG	TCT GCT GCT	GGG TCA TCA	AGT	595
CCT CCC CAG	AGT CCT CAG	GGA GGC GCT	TCC TCC TCC	ATT TCC	637
GTC TAC TAC	ACT TTA TGG	AGC CAA TTC	GAT GAG GGC	TCC AGC	679
AGT CAA GAA	GAG GAA GAG	CCA AGC TCC	TCG GTC GAC	CCA GCT	721
CAG CTG GAG	TTC ATG TTC	CAA GAA GCA	CTG AAA TTG	AAG GTG	763
GCT GAG TTG	GTT CAT TTC	CTG CTC CAC	AAA TAT CGA	GTC AAG	805
GAG CCG GTC	ACA AAG GCA	GAA ATG CTG	GAG AGC GTC	ATC AAA	847
AAT TAC AAG	CGC TAC TTT	CCT GTG ATC	TTC GGC AAA	GCC TCC	889
GAG TTC ATG	CAG GTG ATC	TTT GGC ACT	GAT GTG AAG	GAG GTG	931
GAC CCC GCC	GGC CAC TCC	TAC ATC CTT	GTC ACT GCT	CTT GGC	973
CTC TCG TGC	GAT AGC ATG	CTG GGT GAT	GGT CAT AGC	ATG CCC	1015
AAG GCC GCC	CTC CTG ATC	ATT GTC CTG	GGT GTG ATC	CTA ACC	1057
AAA GAC AAC	TGC GCC CCT	GAA GAG GTT	ATC TGG GAA	GCG TTG	1099
AGT GTG ATG	GGG GTG TAT	GTT GGG AAG	GAG CAC ATG	TTC TAC	1141
GGG GAG CCC	AGG AAG CTG	CTC ACC CAA	GAT TGG GTG	CAG GAA	1183
AAC TAC CTG	GAG TAC CGG	CAG GTG CCC	GGC AGT GAT	CCT GCG	1225
CAC TAC GAG	TTC CTG TGG	GGT TCC AAG	GCC CAC GCT	GAA ACC	1267
AGC TAT GAG	AAG GTC ATA	AAT TAT TTG	GTC ATG CTC	AAT GCA	1309
AGA GAG CCC	ATC TGC TAC	CCA TCC CTT	TAT GAA GAG	GTT TTG	1351
GGA GAG GAG	CAA GAG GGA	GTC TGA			1375
GCACCAGCCG	CAGCCGGGGC	CAAAGTTTGT	GGGGTCA		1412

(2) INFORMATION FOR SEQUENCE ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 920 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-10 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ACCTGCTCCA	GGACAAAGTG	GACCCCACTG	CATCAGCTCC	ACCTACCCTA	50
CTGTCTAGTCC	TGGAGCCTTG	GCCTCTGCCG	GCTGCATCCT	GAGGAGCCAT	100
CTCTCACTTC	CTTCTTCAGG	TTCTCAGGGG	ACAGGGAGAG	CAAGAGGTCA	150
AGAGCTGTGG	GACACCACAG	AGCAGCACTG	AAGGAGAAGA	CCTGTAAGTT	200
GGCCTTTGTT	AGAACCTCCA	GGGTGTGGTT	CTCAGCTGTG	GCCACTTACA	250
CCCTCCCTCT	CTCCCCAGGC	CTGTGGGTCC	CCATCGCCCA	AGTCCTGCCC	300
ACACTCCAC	CTGCTACCCT	GATCAGAGTC	ATC		333
ATG CCT CGA	GCT CCA AAG	CGT CAG CGC	TGC ATG CCT	GAA GAA	375
GAT CTT CAA	TCC CAA AGT	GAG ACA CAG	GGC CTC GAG	GGT GCA	417
CAG GCT CCC	CTG GCT GTG	GAG GAG GAT	GCT TCA TCA	TCC ACT	459

TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC TCC TCC TCC	501
TCT TCC TCC TCC TCC TCC TGC TAT CCT CTA ATA CCA AGC ACC	543
CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA AAT CCT CCC	585
CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCG GTC GTT GCT	627
TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC AGC AGC CAA	669
AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTG CCA GAC AGT	711
GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAG GTG ACT GAT	753
TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATG AAG GAG CCG	795
ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA AAA AAT TAT	837
GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC TCC GAG TGC	879
ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA GTG GAT CC	920

(2) INFORMATION FOR SEQUENCE ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: MAGI-11 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT	50
CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT	100
CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG	150
GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG	200
AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG	250
CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC	300
AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC	350
ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC	400
TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC	450
TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG	500
CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA	550
GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT	600
GATCACAAAG GCAGAA	616
ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT	658
GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT	700
GGC ATT GAT GTG AAG GAA GTG GAC CCC ACT AGC CAC TCC TAT	742
GTC CTT GTC ACC TCC CTC AAC CTC TCT TAT GAT GGC ATA CAG	784
TGT AAT GAG CAG AGC ATG CCC AAG TCT GGC CTC CTG ATA ATA	826
GTC CTG GGT GTA ATC TTC ATG GAG GGG AAC TGC ATC CCT GAA	868
GAG GTT ATG TGG GAA GTC CTG AGC ATT ATG GGG GTG TAT GCT	910
GGA AGG GAG CAC TTC CTC TTT GGG GAG CCC AAG AGG CTC CTT	952
ACC CAA AAT TGG GTG CAG GAA AAG TAC CTG GTG TAC CGG CAG	994
GTG CCC GGC ACT GAT CCT GCA TGC TAT GAG TTC CTG TGG GGT	1036
CCA AGG GCC CAC GCT GAG ACC AGC AAG ATG AAA GTT CTT GAG	1078
TAC ATA GCC AAT GCC AAT GGG AGG GAT CC	1107

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(2) INFORMATION FOR SEQUENCE ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: smage-I

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

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TCTGTCTGCA	TATGCCTCCA	CTTGTGTGTA	GCAGTCTCAA	ATGGATCTCT	50
CTCTACAGAC	CTCTGTCTGT	GTCTGGCACC	CTAAGTGGCT	TTGCATGGGC	100
ACAGGTTTCT	GCCCCTGCAT	GGAGCTTAAA	TAGATCTTTC	TCCACAGGCC	150
TATACCCCTG	CATTGTAAGT	TTAAGTGGCT	TTATGTGGAT	ACAGGTCTCT	200
GCCCTTGTAT	GCAGGCCTAA	GTTTTTCTGT	CTGCTTAACC	CCTCCAAGTG	250
AAGCTAGTGA	AAGATCTAAC	CCACTTTTGG	AAGTCTGAAA	CTAGACTTTT	300
ATGCAGTGGC	CTAACAAGTT	TTAATTTCTT	CCACAGGGTT	TGCAGAAAAG	350
AGCTTGATCC	ACGAGTTCAG	AAGTCCTGGT	ATGTTCTAG	AAAG	394
ATG TTC TCC	TGG AAA GCT	TCA AAA GCC	AGG TCT CCA	TTA AGT	436
CCA AGG TAT	TCT CTA CCT	GGT AGT ACA	GAG GTA CTT	ACA GGT	478
TGT CAT TCT	TAT CCT TCC	AGA TTC CTG	TCT GCC AGC	TCT TTT	520
ACT TCA GCC	CTG AGC ACA	GTC AAC ATG	CCT AGG GGT	CAA AAG	562
AGT AAG ACC	CGC TCC CGT	GCA AAA CGA	CAG CAG TCA	CGC AGG	604
GAG GTT CCA	GTA GTT CAG	CCC ACT GCA	GAG GAA GCA	GGG TCT	646
TCT CCT GTT	GAC CAG AGT	GCT GGG TCC	AGC TTC CCT	GGT GGT	688
TCT GCT CCT	CAG GGT GTG	AAA ACC CCT	GGA TCT TTT	GGT GCA	730
GGT GTA TCC	TGC ACA GGC	TCT GGT ATA	GGT GGT AGA	AAT GCT	772
GCT GTC CTG	CCT GAT ACA	AAA AGT TCA	GAT GGC ACC	CAG GCA	814
GGG ACT TCC	ATT CAG CAC	ACA CTG AAA	GAT CCT ATC	ATG AGG	856
AAG GCT AGT	GTG CTG ATA	GAA TTC CTG	CTA GAT AAA	TTT AAG	898
ATG AAA GAA	GCA GTT ACA	AGG AGT GAA	ATG CTG GCA	GTA GTT	940
AAC AAG AAG	TAT AAG GAG	CAA TTC CCT	GAG ATC CTC	AGG AGA	982
ACT TCT GCA	CGC CTA GAA	TTA GTC TTT	GGT CTT GAG	TTG AAG	1024
GAA ATT GAT	CCC AGC ACT	CAT TCC TAT	TTG CTG GTA	GGC AAA	1066
CTG GGT CTT	TCC ACT GAG	GGA AGT TTG	AGT AGT AAC	TGG GGG	1108
TTG CCT AGG	ACA GGT CTC	CTA ATG TCT	GTC CTA GGT	GTG ATC	1150
TTC ATG AAG	GGT AAC CGT	GCC ACT GAG	CAA GAG GTC	TGG CAA	1192
TTT CTG CAT	GGA GTG GGG	GTA TAT GCT	GGG AAG AAG	CAC TTG	1234
ATC TTT GGC	GAG CCT GAG	GAG TTT ATA	AGA GAT GTA	GTG CGG	1276
GAA AAT TAC	CTG GAG TAC	CGC CAG GTA	CCT GGC AGT	GAT CCC	1318
CCA AGC TAT	GAG TTC CTG	TGG GGA CCC	AGA GCC CAT	GCT GAA	1360
ACA ACC AAG	ATG AAA GTC	CTG GAA GTT	TTA GCT AAA	GTC AAT	1402
GGC ACA GTC	CCT AGT GCC	TTC CCT AAT	CTC TAC CAG	TTG GCT	1444
CTT AGA GAT	CAG GCA GGA	GGG GTG CCA	AGA AGG AGA	GTT CAA	1486
GGC AAG GGT	GTT CAT TCC	AAG GCC CCA	TCC CAA AAG	TCC TCT	1528
AAC ATG TAG					1537
TTGAGTCTGT	TCTGTTGTGT	TTGAAAAACA	GTCAGGCTCC	TAATCAGTAG	1587
AGAGTTCATA	GCCTACCAGA	ACCAACATGC	ATCCATTCTT	GGCCTGTTAT	1637
ACATTAGTAG	AATGGAGGCT	ATTTTGTGTA	CTTTTCAAAT	GTTTGTTTAA	1687
CTAAACAGTG	CTTTTGGCCA	TGCTTCTTGT	TAACCTGCATA	AAGAGGTAAC	1737

TGTCACTTGT	CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
ACATTATTTT	GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTCATG	GCAATGTGAT	ATCATAACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA	TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTTC	TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTTACTC	AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
TTATTTTCTT	CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG	ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG	TCT				2150

(2) INFORMATION FOR SEQUENCE ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2099 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

(A) NAME/KEY: smage-II

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGCC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCTTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCCTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTTCAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCTTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA	ATTAGTCTTT	GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCCT	ATTTGCTGGT	AGGCAAACCTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAC	AGGTCTCCTA	ATGTCTGTCC	1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	CCACTGAGCA	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC	ACTTGATCTT	1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	AATTACCTGG	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCCCTGTGG	1350
GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTT	1400
AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450
TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500

00019669.031797

AAGGGTG TTC	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
GAGTCTG TTC	TGTTGTG TTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
ATTAGTAGAA	TGGAGGCTAT	TTTTGT TACT	TTTCAAATGT	TTGTTTAACT	1700
AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAACTG	1750
TCACTTGTCA	GATTAGGACT	TGTTTTGTTA	TTTGCAACAA	ACTGGAAAAC	1800
ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTTGATGA	2000
CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACTCTA	TTACTTTATT	2050
ATTTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

(2) INFORMATION FOR SEQUENCE ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9 amino acids

(B) TYPE: amino acids

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Boon, Thierry; van der Bruggen, Pierre;
Van den Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne;
Lurquin, Christophe; Chomez, Patrick; Traversari, Catia

(ii) TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS, TUMOR
REJECTION ANTIGENS AND USES THEREOF

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Fulbright & Jaworski L.L.P.
(B) STREET: 666 Fifth Avenue
(C) CITY: New York City
(D) STATE: New York
(F) ZIP: 10103

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/819,669
(B) FILING DATE: March 17, 1997

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/142,368
(B) FILING DATE: May 2, 1994

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/807,043
(B) FILING DATE: December 12, 1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/764,364
(B) FILING DATE: September 23, 1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/728,838
(B) FILING DATE: July 8, 1991

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 07/705,702
(B) FILING DATE: May 23, 1991

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hanson, Norman D.
(B) REGISTRATION NUMBER: 30,946
(C) REFERENCE/DOCKET NUMBER: LUD 5253.5 DIV. - JEL/NDH

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 318-3000
(B) TELEFAX: (212) 752-5958

(2) INFORMATION FOR SEQUENCE ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60
ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTATCCCT CAGCCAATGA GCTTACTGTT 120
CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG 180
CTTGTGAATT TGTACCCCTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240
CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG CATGCATTGT 360
GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG CTAGCTTGGG ACTCTACTCT 420
TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462

(2) INFORMATION FOR SEQUENCE ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 675 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA GGT GGT 48
Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly
5 10 15
GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA 96
Asp Gly Asp Gly Asn Arg Cys Asn Leu Leu His Arg Tyr Ser Leu Glu
20 25 30
GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC TTC GCT GTT GTC ACA ACA 144
Glu Ile Leu Pro Tyr Leu Gly Trp Leu Val Phe Ala Val Val Thr Thr
35 40 45
AGT TTT CTG GCG CTC CAG ATG TTC ATA GAC GCC CTT TAT GAG GAG CAG 192
Ser Phe Leu Ala Leu Gln Met Phe Ile Asp Ala Leu Tyr Glu Glu Gln
50 55 60
TAT GAA AGG GAT GTG GGC TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC 240
Tyr Glu Arg Asp Val Ala Trp Ile Ala Arg Gln Ser Lys Arg Met Ser
65 70 75 80
TCT GTC GAT GAG GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC 288
Ser Val Asp Glu Asp Glu Asp Asp Glu Asp Asp Glu Asp Asp Tyr Tyr
85 90 95
GAC GAC GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 336
Asp Asp Glu Asp Asp Asp Asp Ala Phe Tyr Asp Asp Glu Asp Asp
100 105 110
GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA GAT GAG 384
Glu Glu Glu Glu Leu Glu Asn Leu Met Asp Asp Glu Ser Glu Asp Glu
115 120 125
GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA GCT GAG GAA ATG 432

Ala Glu Glu Glu Met Ser Val Glu Met Gly Ala Gly Ala Glu Glu Met
 130 135 140
 GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT GGC CAT CAT TTA AGG AAG 480
 Gly Ala Gly Ala Asn Cys Ala Cys Val Pro Gly His His Leu Arg Lys
 145 150 155 160
 AAT GAA GTG AAG TGT AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC 528
 Asn Glu Val Lys Cys Arg Met Ile Tyr Phe Phe His Asp Pro Asn Phe
 165 170 175
 CTG GTG TCT ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT 576
 Leu Val Ser Ile Pro Val Asn Pro Lys Glu Gln Met Glu Cys Arg Cys
 180 185 190
 GAA AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA GAG 624
 Glu Asn Ala Asp Glu Glu Val Ala Met Glu Glu Glu Glu Glu Glu Glu
 195 200 205
 GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 672
 Glu Glu Glu Glu Glu Glu Glu Met Gly Asn Pro Asp Gly Phe Ser Pro
 210 215 220 225
 TAG 675

- (2) INFORMATION FOR SEQUENCE ID NO: 3:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 228 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG TTGTTTTTTT 60
 TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA ATTTGATTTT GTTCTAAAGT 120
 TCATTATGCA AAGATGTCAC CAACAGACTT CTGACTGCAT GGTGAACCTT CATATGATAC 180
 ATAGGATTAC ACTTGACCT GTTAAAAATA AAAGTTTGAC TTGCATAC 228

- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1365 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCCG 400
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
 ACCCTTTGTG CC 462

ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC TGT GTT CCT 924
 GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT AGG ATG ATT 966
 TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA GTG 1008
 AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT GAT 1050
 GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAG GAG GAG 1092
 GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA CCT 1134
 TAG 1137
 GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTGG 1187
 TTGTTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGAAA 1237
 ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACTT 1287
 CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACCT 1337
 GTTAAAAATA AAAGTTTGAC TTGCATAC 1365

- (2) INFORMATION FOR SEQUENCE ID NO: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4698 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT 50
 GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT 100
 CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG 150
 AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTTT 200
 CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCCA 250
 CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300
 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCAG 350
 CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCAAG AAGTAAGCCG 400
 CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGGT 450
 ACCCTTTGTG CC 462
 ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC TCA 504
 GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG 546
 TAC TCC CTG GAA GAA ATT CTG CCT TAT CTA GGG TGG CTG GTC 588
 TTC GCT GTT GTC ACA ACA AGT TTT CTG GCG CTC CAG ATG TTC 630
 ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GAT GTG GCC 672
 TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT GAG 714
 GAT GAA GAC GAT GAG GAT GAT GAG GAT GAC TAC TAC GAC GAC 756
 GAG GAC GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT GAT 798
 GAG GAA GAA GAA TTG GAG AAC CTG ATG GAT GAT GAA TCA GAA 840
 GAT GAG GCC GAA GAA GAG ATG AGC GTG GAA ATG GGT GCC GGA 882
 GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T 916

GTGAGTAACC CGTGGTCTTT ACTCTAGATT CAGGTGGGGT GCATTCTTTA 966
 CTCTTGCCCA CATCTGTAGT AAAGACCACA TTTTGGTTGG GGGTCATTGC 1016
 TGGAGCCATT CCTGGCTCTC CTGTCCACGC CTATCCCCGC TCCTCCCATC 1066
 CCCCACCTCT TGCTCCGCTC TCTTTCCTTT TCCCACCTTG CCTCTGGAGC 1116
 TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CTTGCTCCCC 1166
 TCCCCCTCGG CTCAACTTTT CGTGCCTTCT GCTCTCTGAT CCCCACCCTC 1216
 TTCAGGCTTC CCCATTTGCT CCTCTCCCGA AACCTCCCC TTCCTGTTCC 1266
 CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TATTTACCTT 1316
 TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CCTTTTCTTT 1366
 TCCTGCTCCC CTCCCCCTCC CCTCCCTGTT TACCCTTCAC CGCTTTTCCT 1416
 CTACCTGCTT CCCTCCCCCT TGCTGCTCCC TCCCTATTTG CATTTTTCGGG 1466
 TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TTCGGGTGCT 1516
 CCTCCCTCCC CCTCCCCAGG CCTTTTTTTTT TTTTTTTTTT TTTTTTTTTT 1566
 TTGGTTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GTCCTGGCAC 1616
 TCACTCTGTA GACCAGGCTG GCCTCAAAC CAGAAATCTG CCTGCCTCTG 1666
 CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CCCAGTGCAG 1716
 GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TCTGCATGTT 1766
 AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CCCTCCCTGT 1816
 TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TCCCTGCTCC 1866
 CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CCTGCTTTCT 1916
 GCCCGTTCC CTTTTTTTGT GCCTTTCCTC CTGGCTCCCC TCCACCTTCC 1966
 AGCTCACCTT TTTGTTTGTG TGTTTGTGTT GTTGTGTTGGT TTGCTTTTTT 2016
 TTTTTTTTTT GCACCTTGTT TTCCAAGATC CCCCTCCCC TCCGGCTTCC 2066
 CCTCTGTGTG CCTTTCCTGT TCCCTCCCC TCGCTGGCTC CCCCTCCCTT 2116
 TCTGCCTTTC CTGTCCCTGC TCCCTTCTCT GCTAACCTTT TAATGCCTTT 2166
 CTTTTCTAGA CTCCCCCTC CAGGCTTGCT GTTTGCTTCT GTGCACTTTT 2216
 CCTGACCCTG CTCCCCTTCC CCTCCCAGCT CCCCCCTCTT TTCCCACCTC 2266
 CCTTTCTCCA GCCTGTCACC CCTCCTTCTC TCCTCTCTGT TTCTCCCACT 2316
 TCCTGCTTCC TTTACCCCTT CCCTCTCCCT ACTCTCCTCC CTGCCTGCTG 2366
 GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC 2416
 CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT 2466
 ATGTGTCTCT CTTCTATCT ATCCCTTCTT TTCTGTCCCC TCTCCTCTGT 2516
 CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA 2566
 CCTGCTTCTT TACCCTGCCT CTCCCATGCT CCTCTTACCT TTATGCCCAT 2616
 TCCATGTCCC CTCTCAATT CCGTGTCCAT TGTGCTCCCT CACATCTTCC 2666
 ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC 2716
 TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC 2766
 TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC 2816
 CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC 2866
 ATCAACAACA AGGAGGCAAG AAACAGAGCA AAATCCCAA ATCAGCAGGA 2916
 AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC 2966
 AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT 3016
 CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG 3066
 CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA 3116
 GAATCTGAAA ACTAGGGGCC AGTGGTTTTGT TTTGGGGACA AATTAGCACG 3166
 TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA 3216
 TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA 3266
 GGCTAAAGAT ACTTGAAGCC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT 3316
 TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG 3355
 GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT 3396
 AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT 3438
 ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA 3480
 AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA GAA 3522
 GAG GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC 3564

TTC TCA CCT TAG 3576
 GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA 3626
 GCTAAGAGCA TCTTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA 3676
 TCTTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA 3726
 CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT 3776
 GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA 3826
 GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG 3876
 TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT 3926
 TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG 3976
 TTCTGATTTT TTTTATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT 4026
 CTTAAAATTT CTTTCATCTT TAATTTTCTT TAACCTTTAGT TTTTTTCACT 4076
 TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTGA GATTTCTTAA 4126
 AATGTTTTTTT AAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA 4176
 GTAACGGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA 4226
 GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC 4276
 CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC 4326
 ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT 4376
 ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA 4426
 AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC 4476
 AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT 4526
 TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA 4576
 TTTTGTTCTA AAGTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT 4626
 GCATGGTGAA CTTTCATATG ATACATAGGA TTACACTTGT ACCTGTTAAA 4676
 AATAAAAGTT TGACTTGCAT AC 4698

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu
 5

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2420 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC CCTGCCAGGA AAAATATAAG GGCCCTGCGT GAGAACAGAG 50
 GGGGTCATCC ACTGCATGAG AGTGGGGATG TCACAGAGTC CAGCCCACCC 100
 TCCTGGTAGC ACTGAGAAGC CAGGGCTGTG CTTGCGGTCT GCACCCTGAG 150
 GGCCCGTGGA TTCCTCTTCC TGGAGCTCCA GGAACCAGGC AGTGAGGCCT 200
 TGGTCTGAGA CAGTATCCTC AGGTCACAGA GCAGAGGATG CACAGGGTGT 250
 GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA 300

CAGGACACAT AGGACTCCAC AGAGTCTGGC CTCACCTCCC TACTGTCAGT 350
 CCTGTAGAAT CGACCTCTGC TGGCCGGCTG TACCCTGAGT ACCCTCTCAC 400
 TTCCTCCTTC AGGTTTTTCAG GGGACAGGCC AACCAGAGG ACAGGATTCC 450
 CTGGAGGCCA CAGAGGAGCA CCAAGGAGAA GATCTGTAAG TAGGCCTTTG 500
 TTAGAGTCTC CAAGGTTTCAG TTCTCAGCTG AGGCCTCTCA CACACTCCCT 550
 CTCTCCCCAG GCCTGTGGGT CTTATTGCC CAGCTCCTGC CCACACTCCT 600
 GCCTGCTGCC CTGACGAGAG TCATCATGTC TCTTGAGCAG AGGAGTCTGC 650
 ACTGCAAGCC TGAGGAAGCC CTTGAGGCC AACAAGAGGC CCTGGGCCTG 700
 GTGTGTGTGC AGGCTGCCAC CTCCTCCTCC TCTCCTCTGG TCCTGGGCAC 750
 CCTGGAGGAG GTGCCCACTG CTGGGTCAAC AGATCCTCCC CAGAGTCCTC 800
 AGGGAGCCTC CGCCTTTCCC ACTACCATCA ACTTCACTCG ACAGAGGCAA 850
 CCCAGTGAGG GTTCCAGCAG CCGTGAAGAG GAGGGGCCAA GCACCTCTTG 900
 TATCCTGGAG TCCTTGTTCC GAGCAGTAAT CACTAAGAAG GTGGCTGATT 950
 TGGTTGGTTT TCTGCTCCTC AAATATCGAG CCAGGGAGCC AGTCACAAAG 1000
 GCAGAAATGC TGGAGAGTGT CATCAAAAAT TACAAGCACT GTTTTCCTGA 1050
 GATCTTCGGC AAAGCCTCTG AGTCCTTGCA GCTGGTCTTT GGCATTGACG 1100
 TGAAGGAAGC AGACCCACCC GGCCACTCCT ATGTCCTTGT CACCTGCCTA 1150
 GGTCTCTCCT ATGATGGCCT GCTGGGTGAT AATCAGATCA TGCCCAAGAC 1200
 AGGCTTCCTG ATAATTGTCC TGGTCATGAT TGCAATGGAG GCGGCCCATG 1250
 CTCTGAGGA GGAAATCTGG GAGGAGCTGA GTGTGATGGA GGTGTATGAT 1300
 GGGAGGGAGC ACAGTGCCCTA TGGGGAGCCC AGGAAGCTGC TCACCCAAGA 1350
 TTTGGTGCAG GAAAAGTACC TGGAGTACCG GCAGGTGCCG GACAGTGATC 1400
 CCGCACGCTA TGAGTTCCTG TGGGGTCCAA GGGCCCTCGC TGAAACCAGC 1450
 TATGTGAAAG TCCTTGAGTA TGTGATCAAG GTCAGTGCAA GAGTTCGCTT 1500
 TTTCTTCCCA TCCCTGCGTG AAGCAGCTTT GAGAGAGGAG GAAGAGGGAG 1550
 TCTGAGCATG AGTTGCAGCC AAGGCCAGTG GGAGGGGGAC TGGGCCAGTG 1600
 CACCTTCCAG GGCCGCGTCC AGCAGCTTCC CCTGCCTCGT GTGACATGAG 1650
 GCCCATTCTT CACTCTGAAG AGAGCGGTCA GTGTTCTCAG TAGTAGGTTT 1700
 CTGTTCTATT GGGTGA CTG GAGATTTATC TTTGTTCTCT TTTGGAATTG 1750
 TTCAAATGTT TTTTTTTAAG GGATGGTTGA ATGAACTTCA GCATCCAAGT 1800
 TTATGAATGA CAGCAGTCAC ACAGTTCCTGT GTATATAGTT TAAGGGTAAG 1850
 AGTCTTGTGT TTTATTGAGA TTGGGAAATC CATTCTATTT TGTGAATTGG 1900
 GATAATAACA GCAGTGGAAT AAGTACTTAG AAATGTGAAA AATGAGCAGT 1950
 AAAATAGATG AGATAAAGAA CTAAAGAAAT TAAGAGATAG TCAATTCTTG 2000
 CCTTATACCT CAGTCTATTG TGTAATAATTT TAAAGATAT ATGCATACCT 2050
 GGATTTCTTT GGCTTCTTTG AGAATGTAAG AGAAATTAAA TCTGAATAAA 2100
 GAATTCTTCC TGTTCACTGG CTCTTTTCTT CTCCATGCAC TGAGCATCTG 2150
 CTTTTTGGAA GGCCCTGGGT TAGTAGTGGA GATGCTAAGG TAAGCCAGAC 2200
 TCATACCCAC CCATAGGGTC GTAGAGTCTA GGAGCTGCAG TCACGTAATC 2250
 GAGGTGGCAA GATGTCTCT AAAGATGTAG GGAAAAGTGA GAGAGGGGTG 2300
 AGGGTGTGGG GCTCCGGGTG AGAGTGGTGG AGTGTCAATG CCCTGAGCTG 2350
 GGGCATTTTG GGCTTTGGGA AACTGCAGTT CTTCTGGGG GAGCTGATTG 2400
 TAATGATCTT GGGTGGATCC 2420

(2) INFORMATION FOR SEQUENCE ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5675 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-1 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCCGGGGCAC CACTGGCATC CCTCCCCCTA CCACCCCCAA TCCCTCCCTT 50
TACGCCACCC ATCCAAACAT CTTACGCTC ACCCCAGCC CAAGCCAGGC 100
AGAATCCGGT TCCACCCCTG CTCTCAACCC AGGGAAGCCC AGGTGCCCAG 150
ATGTGACGCC ACTGACTTGA GCATTAGTGG TTAGAGAGAA GCGAGGTTTT 200
CGGTCTGAGG GGCGGCTTGA GATCGGTGGA GGGAAGCGGG CCCAGCTCTG 250
TAAGGAGGCA AGGTGACATG CTGAGGGAGG ACTGAGGACC CACTTACCCC 300
AGATAGAGGA CCCCAAATAA TCCCTTCATG CCAGTCCTGG ACCATCTGGT 350
GGTGGACTTC TCAGGCTGGG CCACCCCAG CCCCTTGCT GCTTAAACCA 400
CTGGGGACTC GAAGTCAGAG CTCCGTGTGA TCAGGGAAGG GCTGCTTAGG 450
AGAGGGCAGC GTCCAGGCTC TGCCAGACAT CATGCTCAGG ATTCTCAAGG 500
AGGGCTGAGG GTCCCTAAGA CCCCACTCCC GTGACCCAAC CCCCACTCCA 550
ATGCTCACTC CCGTGACCCA ACCCCCTCTT CATTGTCTATT CCAACCCCCA 600
CCCCACATCC CCCACCCCAT CCCTCAACCC TGATGCCCAT CCGCCCAGCC 650
ATTCCACCCT CACCCCCACC CCCACCCCCA CGCCCACTCC CACCCCCACC 700
CAGGCAGGAT CCGGTTCCCCG CCAGGAAACA TCCGGGTGCC CGGATGTGAC 750
GCCACTGACT TGCGCATTGT GGGGCAGAGA GAAGCGAGGT TTCCATTCTG 800
AGGGACGGCG TAGAGTTCGG CCGAAGGAAC CTGACCCAGG CTCTGTGAGG 850
AGGCAAGGTG AGAGGCTGAG GGAGGACTGA GGACCCCGCC ACTCCAAATA 900
GAGAGCCCCA AATATTCCAG CCCCGCCCTT GCTGCCAGCC CTGGCCCACC 950
CGCGGGAAGA CGTCTCAGCC TGGGCTGCCC CCAGACCCCT GCTCCAAAAG 1000
CCTTGAGAGA CACCAGGTTT TTCTCCCCAA GCTCTGGAAT CAGAGGTTGC 1050
TGTGACCAGG GCAGGACTGG TTAGGAGAGG GCAGGGCACA GGCTCTGCCA 1100
GGCATCAAGA TCAGCACCCA AGAGGGAGGG CTGTGGGCCC CCAAGACTGC 1150
ACTCCAATCC CCACTCCAC CCCATTGCA TTCCCATTC CCACCCAACC 1200
CCCATCTCCT CAGCTACACC TCCACCCCCA TCCCTACTCC TACTCCGTCA 1250
CCTGACCACC ACCCTCCAGC CCCAGCACCA GCCCCAACC TTCTGCCACC 1300
TCACCCTCAC TGCCCCCAAC CCCACCTCA TCTCTCTCAT GTGCCCCACT 1350
CCCATCGCCT CCCCCATTCT GGCAGAATCC GGTTTGCCCC TGCTCTCAAC 1400
CCAGGGAAGC CCTGGTAGGC CCGATGTGAA ACCACTGACT TGAACCTCAC 1450
AGATCTGAGA GAAGCCAGGT TCATTTAATG GTTCTGAGGG GCGGCTTGAG 1500
ATCCACTGAG GGGAGTGGTT TTAGGCTCTG TGAGGAGGCA AGGTGAGATG 1550
CTGAGGGAGG ACTGAGGAGG CACACACCCC AGGTAGATGG CCCCCAAATG 1600
ATCCAGTACC ACCCTGCTG CCAGCCCTGG ACCACCCGGC CAGGACAGAT 1650
GTCTCAGCTG GACCACCCCC CGTCCCCTCC CACTGCCACT TAACCCACAG 1700
GGCAATCTGT AGTCATAGCT TATGTGACCG GGGCAGGGTT GGTGAGGAGA 1750
GGCAGGGCCC AGGCATCAAG GTCCAGCATC CGCCCGGCAT TAGGGTCAGG 1800
ACCCTGGGAG GGAAGTGAAG GTTCCCCACC CACACCTGTC TCCTCATCTC 1850
CACCGCCACC CCACTCACAT TCCCATACCT ACCCCCTACC CCCAACCTCA 1900
TCTTGTCAGA ATCCCTGCTG TCAACCCACG GAAGCCACGG GAATGGCGGC 1950
CAGGCACTCG GATCTTGACG TCCCCATCCA GGGTCTGATG GAGGGAAGGG 2000
GCTTGAACAG GGCCTCAGGG GAGCAGAGGG AGGGCCCTAC TGCGAGATGA 2050
GGGAGGCCTC AGAGGACCCA GCACCCTAGG ACACCGCACC CCTGTCTGAG 2100
ACTGAGGCTG CCACTTCTGG CCTCAAGAAT CAGAACGATG GGGACTCAGA 2150
TTGCATGGGG GTGGGACCCA GGCCTGCAAG GCTTACGCGG AGGAAGAGGA 2200
GGGAGGACTC AGGGGACCTT GGAATCCAGA TCAGTGTGGA CCTCGGCCCT 2250
GAGAGGTCCA GGGCACGGTG GCCACATATG GCCCATATTT CCTGCATCTT 2300
TGAGGTGACA GGACAGAGCT GTGGTCTGAG AAGTGGGGCC TCAGGTCAAC 2350
AGAGGGAGGA GTTCCAGGAT CCATATGGCC CAAGATGTGC CCCCTTCATG 2400
AGGACTGGGG ATATCCCCGG CTCAGAAAGA AGGGACTCCA CACAGTCTGG 2450
CTGTCCCCTT TTAGTAGCTC TAGGGGGACC AGATCAGGGA TGGCGGTATG 2500
TTCCATTCTC ACTTGTAACA CAGGCAGGAA GTTGGGGGGC CCTCAGGGAG 2550
ATGGGGTCTT GGGGTAAAGG GGGGATGTCT ACTCATGTCA GGGAAATTGGG 2600

GGTTGAGGAA	GCACAGGCGC	TGGCAGGAAT	AAAGATGAGT	GAGACAGACA	2650
AGGCTATTGG	AATCCACACC	CCAGAACCAA	AGGGGTCAGC	CCTGGACACC	2700
TCACCCAGGA	TGTGGCTTCT	TTTTCACTCC	TGTTTCCAGA	TCTGGGGCAG	2750
GTGAGGACCT	CATTCTCAGA	GGGTGACTCA	GGTCAACGTA	GGGACCCCCA	2800
TCTGGTCTAA	AGACAGAGCG	GTCCCAGGAT	CTGCCATGCG	TTCGGGTGAG	2850
GAACATGAGG	GAGGACTGAG	GGTACCCCAG	GACCAGAACA	CTGAGGGAGA	2900
CTGCACAGAA	ATCAGCCCTG	CCCCTGCTGT	CACCCCAGAG	AGCATGGGCT	2950
GGGCCGTCTG	CCGAGGTCTT	TCCGTTATCC	TGGGATCATT	GATGTCAGGG	3000
ACGGGGAGGC	CTTGGTCTGA	GAAGGCTGCG	CTCAGGTCAG	TAGAGGGAGC	3050
GTCCCAGGCC	CTGCCAGGAG	TCAAGGTGAG	GACCAAGCGG	GCACCTCACC	3100
CAGGACACAT	TAATTCCAAT	GAATTTTGAT	ATCTCTTGCT	GCCCTTCCCC	3150
AAGGACCTAG	GCACGTGTGG	CCAGATGTTT	GTCCCCTCCT	GTCCTTCCAT	3200
TCCTTATCAT	GGATGTGAAC	TCTTGATTTG	GATTTCTCAG	ACCAGCAAAA	3250
GGGCAGGATC	CAGGCCCTGC	CAGGAAAAAT	ATAAGGGCCC	TGCGTGAGAA	3300
CAGAGGGGGT	CATCCACTGC	ATGAGAGTGG	GGATGTCACA	GAGTCCAGCC	3350
CACCCTCCTG	GTAGCACTGA	GAAGCCAGGG	CTGTGCTTGC	GGTCTGCACC	3400
CTGAGGGCCC	GTGGATTCTT	CTTCCTGGAG	CTCCAGGAAC	CAGGCAGTGA	3450
GGCCTTGGTC	TGAGACAGTA	TCCTCAGGTC	ACAGAGCAGA	GGATGCACAG	3500
GGTGTGCCAG	CAGTGAATGT	TTGCCCTGAA	TGCACACCAA	GGGCCCCACC	3550
TGCCACAGGA	CACATAGGAC	TCCACAGAGT	CTGGCCTCAC	CTCCCTACTG	3600
TCAGTCCTGT	AGAATCGACC	TCTGCTGGCC	GGCTGTACCC	TGAGTACCCT	3650
CTCACTTCTT	CCTTCAGGTT	TTCAGGGGAC	AGGCCAACCC	AGAGGACAGG	3700
ATTCCCTGGA	GGCCACAGAG	GAGCACCAAG	GAGAAGATCT	GTAAGTAGGC	3750
CTTTGTTAGA	GTCTCCAAGG	TTCAGTTCTC	AGCTGAGGCC	TCTCACACAC	3800
TCCCTCTCTC	CCCAGGCCTG	TGGGTCTTCA	TTGCCCAGCT	CCTGCCCACA	3850
CTCCTGCCTG	CTGCCCTGAC	GAGAGTCATC			3880
ATG TCT CTT	GAG CAG AGG	AGT CTG CAC	TGC AAG CCT	GAG GAA	3922
GCC CTT GAG	GCC CAA CAA	GAG GCC CTG	GGC CTG GTG	TGT GTG	3964
CAG GCT GCC	ACC TCC TCC	TCT CCT CTG	GTC CTG GGC	ACC	4006
CTG GAG GAG	GTG CCC ACT	GCT GGG TCA	ACA GAT CCT	CCC CAG	4048
AGT CCT CAG	GGA GCC TCC	GCC TTT CCC	ACT ACC ATC	AAC TTC	4090
ACT CGA CAG	AGG CAA CCC	AGT GAG GGT	TCC AGC AGC	CGT GAA	4132
GAG GAG GGG	CCA AGC ACC	TCT TGT ATC	CTG GAG TCC	TTG TTC	4174
CGA GCA GTA	ATC ACT AAG	AAG GTG GCT	GAT TTG GTT	GGT TTT	4216
CTG CTC CTC	AAA TAT CGA	GCC AGG GAG	CCA GTC ACA	AAG GCA	4258
GAA ATG CTG	GAG AGT GTC	ATC AAA AAT	TAC AAG CAC	TGT TTT	4300
CCT GAG ATC	TTC GGC AAA	GCC TCT GAG	TCC TTG CAG	CTG GTC	4342
TTT GGC ATT	GAC GTG AAG	GAA GCA GAC	CCC ACC GGC	CAC TCC	4384
TAT GTC CTT	GTC ACC TGC	CTA GGT CTC	TCC TAT GAT	GGC CTG	4426
CTG GGT GAT	AAT CAG ATC	ATG CCC AAG	ACA GGC TTC	CTG ATA	4468
ATT GTC CTG	GTC ATG ATT	GCA ATG GAG	GGC GGC CAT	GCT CCT	4510
GAG GAG GAA	ATC TGG GAG	GAG CTG AGT	GTG ATG GAG	GTG TAT	4552
GAT GGG AGG	GAG CAC AGT	GCC TAT GGG	GAG CCC AGG	AAG CTG	4594
CTC ACC CAA	GAT TTG GTG	CAG GAA AAG	TAC CTG GAG	TAC CGG	4636
CAG GTG CCG	GAC AGT GAT	CCC GCA CGC	TAT GAG TTC	CTG TGG	4678
GGT CCA AGG	GCC CTC GCT	GAA ACC AGC	TAT GTG AAA	GTC CTT	4720
GAG TAT GTG	ATC AAG GTC	AGT GCA AGA	GTT CGC TTT	TTC TTC	4762
CCA TCC CTG	CGT GAA GCA	GCT TTG AGA	GAG GAG GAA	GAG GGA	4804
GTC TGA					4810
GCATGAGTTG	CAGCCAAGGC	CAGTGGGAGG	GGGACTGGGC	CAGTGCACCT	4860
TCCAGGGCCG	CGTCCAGCAG	CTTCCCCTGC	CTCGTGTGAC	ATGAGGCCCA	4910
TTCTTCACTC	TGAAGAGAGC	GGTCAGTGTT	CTCAGTAGTA	GGTTTCTGTT	4960
CTATTGGGTG	ACTTGGAGAT	TTATCTTTGT	TCTCTTTTGG	AATTGTTCAA	5010
ATGTTTTTTTT	TTAAGGGATG	GTTGAATGAA	CTTCAGCATC	CAAGTTTATG	5060

AATGACAGCA	GTCACACAGT	TCTGTGTATA	TAGTTTAAGG	GTAAGAGTCT	5110
TGTGTTTTAT	TCAGATTGGG	AAATCCATTC	TATTTTGTGA	ATTGGGATAA	5160
TAACAGCAGT	GGAATAAGTA	CTTAGAAATG	TGAAAAATGA	GCAGTAAAAT	5210
AGATGAGATA	AAGAACTAAA	GAAATTAAGA	GATAGTCAAT	TCTTGCCTTA	5260
TACCTCAGTC	TATTCTGTAA	AATTTTAAA	GATATATGCA	TACCTGGATT	5310
TCCTTGGCTT	CTTTGAGAAT	GTAAGAGAAA	TTAAATCTGA	ATAAAGAATT	5360
CTTCCTGTTC	ACTGGCTCTT	TTCTTCTCCA	TGCACTGAGC	ATCTGCTTTT	5410
TGGAAGGCCC	TGGGTTAGTA	GTGGAGATGC	TAAGGTAAGC	CAGACTCATA	5460
CCCACCCATA	GGGTCTAGTA	GTCTAGGAGC	TGCAGTCACG	TAATCGAGGT	5510
GGCAAGATGT	CCTCTAAAGA	TGTAGGGAAA	AGTGAGAGAG	GGGTGAGGGT	5560
GTGGGGCTCC	GGGTGAGAGT	GGTGGAGTGT	CAATGCCCTG	AGCTGGGGCA	5610
TTTTGGGCTT	TGGGAAACTG	CAGTTCCTTC	TGGGGGAGCT	GATTGTAATG	5660
ATCTTGGGTG	GATCC				5675

(2) INFORMATION FOR SEQUENCE ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-2 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCCATCCAGA	TCCCCATCCG	GGCAGAATCC	GGTTCCACCC	TTGCCGTGAA	50
CCCAGGGAAG	TCACGGGCCC	GGATGTGACG	CCACTGACTT	GCACATTGGA	100
GGTCAGAGGA	CAGCGAGATT	CTCGCCCTGA	GCAACGGCCT	GACGTCGGCG	150
GAGGGAAGCA	GGCGCAGGCT	CCGTGAGGAG	GCAAGGTAAG	ACGCCGAGGG	200
AGGACTGAGG	CGGGCCTCAC	CCCAGACAGA	GGGCCCCCAA	TTAATCCAGC	250
GCTGCCTCTG	CTGCCGGGCC	TGGACCACCC	TGCAGGGGAA	GACTTCTCAG	300
GCTCAGTCGC	CACCACCTCA	CCCCGCCACC	CCCCGCCGCT	TTAACCGCAG	350
GGAACTCTGG	CGTAAGAGCT	TTGTGTGACC	AGGGCAGGGC	TGGTTAGAAG	400
TGCTCAGGGC	CCAGACTCAG	CCAGGAATCA	AGGTGAGGAC	CCCAAGAGGG	450
GACTGAGGGC	AACCCACCCC	CTACCCTCAC	TACCAATCCC	ATCCCCCAAC	500
ACCAACCCCA	CCCCCATCCC	TCAAACACCA	ACCCACCCC	CAAACCCCAT	550
TCCCATCTCC	TCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
ACGTTACAT	GTACGGCTAA	GGGAGGGAAG	GGGTTGGGTC	TCGTGAGTAT	700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCCTG	TACCCCTGTC	800
TCAAACCTGAG	CCACCTTTTC	ATTGAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACCTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
AAGAGGGAGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTTCAGGG	1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTACCCCTA	GAACCAAAGG	GGTCAGCCCT	1400

GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCTGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
ATCCAGGTGG	AGAGCCTGAG	GTAGGATTGA	GGGTACCCCT	GGGCCAGAAT	1600
GCAGCAAGGG	GGCCCCATAG	AAATCTGCCC	TGCCCCCTGCG	GTTACTTCAG	1650
AGACCCTGGG	CAGGGCTGTC	AGCTGAAGTC	CCTCCATTAT	CTGGGATCTT	1700
TGATGTCAGG	GAAGGGGAGG	CCTTGGTCTG	AAGGGGCTGG	AGTCAGGTCA	1750
GTAGAGGGAG	GGTCTCAGGC	CCTGCCAGGA	GTGGACGTGA	GGACCAAGCG	1800
GACTCGTCAC	CCAGGACACC	TGGACTCCAA	TGAATTTGAC	ATCTCTCGTT	1850
GTCCTTCGCG	GAGGACCTGG	TCACGTATGG	CCAGATGTGG	GTCCCCTCTA	1900
TCTCCTTCTG	TACCATATCA	GGGATGTGAG	TTCTTGACAT	GAGAGATTCT	1950
CAAGCCAGCA	AAAGGGTGGG	ATTAGGCCCT	ACAAGGAGAA	AGGTGAGGGC	2000
CCTGAGTGAG	CACAGAGGGG	ACCCTCCACC	CAAGTAGAGT	GGGGACCTCA	2050
CGGAGTCTGG	CCAACCCTGC	TGAGACTTCT	GGGAATCCGT	GGCTGTGCTT	2100
GCAGTCTGCA	CACTGAAGGC	CCGTGCATTG	CTCTCCCAGG	AATCAGGAGC	2150
TCCAGGAACC	AGGCAGTGAG	GCCTTGGTCT	GAGTCAGTGC	CTCAGGTCAC	2200
AGAGCAGAGG	GGACGCAGAC	AGTGCCAACA	CTGAAGGTTT	GCCTGGAATG	2250
CACACCAAGG	GCCCCACCCG	CCCAGAACAA	ATGGGACTCC	AGAGGGCCTG	2300
GCCTCACCCCT	CCCTATTCTC	AGTCCTGCAG	CCTGAGCATG	TGCTGGCCGG	2350
CTGTACCCTG	AGGTGCCCTC	CCACTTCCTC	CTTCAGGTTT	TGAGGGGGAC	2400
AGGCTGACAA	GTAGGACCCG	AGGCACTGGA	GGAGCATTGA	AGGAGAAGAT	2450
CTGTAAGTAA	GCCTTTGTCA	GAGCCTCCAA	GGTTCAGTTC	AGTTCTCACC	2500
TAAGGCCTCA	CACACGCTCC	TTCTCTCCCC	AGGCCTGTGG	GTCTTCATTG	2550
CCCAGCTCCT	GCCCCGACTC	CTGCCTGCTG	CCCTGACCAG	AGTCATC	2597
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	2639
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	2681
CAG GCT CCT	GCT ACT GAG	GAG CAG CAG	ACC GCT TCT	TCC TCT	2723
TCT ACT CTA	GTG GAA GTT	ACC CTG GGG	GAG GTG CCT	GCT GCC	2765
GAC TCA CCG	AGT CCT CCC	CAC AGT CCT	CAG GGA GCC	TCC AGC	2807
TTC TCG ACT	ACC ATC AAC	TAC ACT CTT	TGG AGA CAA	TCC GAT	2849
GAG GGC TCC	AGC AAC CAA	GAA GAG GAG	GGG CCA AGA	ATG TTT	2891
CCC GAC CTG	GAG TCC GAG	TTC CAA GCA	GCA ATC AGT	AGG AAG	2933
ATG GTT GAG	TTG GTT CAT	TTT CTG CTC	CTC AAG TAT	CGA GCC	2975
AGG GAG CCG	GTC ACA AAG	GCA GAA ATG	CTG GAG AGT	GTC CTC	3017
AGA AAT TGC	CAG GAC TTC	TTT CCC GTG	ATC TTC AGC	AAA GCC	3059
TCC GAG TAC	TTG CAG CTG	GTC TTT GGC	ATC GAG GTG	GTG GAA	3101
GTG GTC CCC	ATC AGC CAC	TTG TAC ATC	CTT GTC ACC	TGC CTG	3143
GGC CTC TCC	TAC GAT GGC	CTG CTG GGC	GAC AAT CAG	GTC ATG	3185
CCC AAG ACA	GGC CTC CTG	ATA ATC GTC	CTG GCC ATA	ATC GCA	3227
ATA GAG GGC	GAC TGT GCC	CCT GAG GAG	AAA ATC TGG	GAG GAG	3269
CTG AGT ATG	TTG GAG GTG	TTT GAG GGG	AGG GAG GAC	AGT GTC	3311
TTC GCA CAT	CCC AGG AAG	CTG CTC ATG	CAA GAT CTG	GTG CAG	3353
GAA AAC TAC	CTG GAG TAC	CGG CAG GTG	CCC GGC AGT	GAT CCT	3395
GCA TGC TAC	GAG TTC CTG	TGG GGT CCA	AGG GCC CTC	ATT GAA	3437
ACC AGC TAT	GTG AAA GTC	CTG CAC CAT	ACA CTA AAG	ATC GGT	3479
GGA GAA CCT	CAC ATT TCC	TAC CCA CCC	CTG CAT GAA	CGG GCT	3521
TTG AGA GAG	GGA GAA GAG	TGA			3542
GTCTCAGCAC	ATGTTGCAGC	CAGGGCCAGT	GGGAGGGGGT	CTGGGCCAGT	3592
GCACCTTCCA	GGGCCCCATC	CATTAGCTTC	CACTGCCTCG	TGTGATATGA	3642
GGCCCATTC	TGCCTCTTTG	AAGAGAGCAG	TCAGCATTCT	TAGCAGTGAG	3692
TTTCTGTTCT	GTTGGATGAC	TTTGAGATTT	ATCTTTCTTT	CCTGTTGGAA	3742
TTGTTCAAAT	GTTCTTTTAA	ACAAATGGTT	GGATGAACTT	CAGCATCCAA	3792
GTTTATGAAT	GACAGTAGTC	ACACATAGTG	CTGTTTATAT	AGTTTAGGGG	3842
TAAGAGTCCT	GTTTTTTATT	CAGATTGGGA	AATCCATTCC	ATTTTGTGAG	3892

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TTGTCACATA	ATAACAGCAG	TGGAATATGT	ATTTGCCTAT	ATTGTGAACG	3942
AATTAGCAGT	AAAATACATG	ATACAAGGAA	CTCAAAAGAT	AGTTAATTCT	3992
TGCCTTATAC	CTCAGTCTAT	TATGTAAAAT	TAAAAATATG	TGTATGTTTT	4042
TGCTTCTTTG	AGAATGCAAA	AGAAATTAAA	TCTGAATAAA	TTCTTCCTGT	4092
TCACTGGCTC	ATTTCTTTAC	CATTCACTCA	GCATCTGCTC	TGTGGAAGGC	4142
CCTGGTAGTA	GTGGG				4157

(2) INFORMATION FOR SEQUENCE ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 662 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-21 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
AGGGAAGTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

(2) INFORMATION FOR SEQUENCE ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1640 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

- (A) NAME/KEY: cDNA MAGE-3

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG	AAGCCGGCCC	AGGCTCGGTG	AGGAGGCAAG	GTTCTGAGGG	50
GACAGGCTGA	CCTGGAGGAC	CAGAGGCCCC	CGGAGGAGCA	CTGAAGGAGA	100
AGATCTGCCA	GTGGGTCTCC	ATTGCCCAGC	TCCTGCCCAC	ACTCCCGCCT	150
GTTGCCCTGA	CCAGAGTCAT	C			171
ATG CCT CTT	GAG CAG AGG	AGT CAG CAC	TGC AAG CCT	GAA GAA	213
GGC CTT GAG	GCC CGA GGA	GAG GCC CTG	GGC CTG GTG	GGT GCG	255
CAG GCT CCT	GCT ACT GAG	GAG CAG GAG	GCT GCC TCC	TCC TCT	297
TCT ACT CTA	GTT GAA GTC	ACC CTG GGG	GAG GTG CCT	GCT GCC	339

GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC 381
 CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT 423
 GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC 465
 CCT GAC CTG GAG TCC GAG TTC CAA GCA GCA CTC AGT AGG AAG 507
 GTG GCC GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC 549
 AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GGG AGT GTC GTC 591
 GGA AAT TGG CAG TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT 633
 TCC AGT TCC TTG CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA 675
 GTG GAC CCC ATC GGC CAC TTG TAC ATC TTT GCC ACC TGC CTG 717
 GGC CTC TCC TAC GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG 759
 CCC AAG GCA GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA 801
 AGA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG 843
 CTG AGT GTG TTA GAG GTG TTT GAG GGG AGG GAA GAC AGT ATG 885
 TTG GGG GAT CCC AAG AAG CTG CTC ACC CAA CAT TTC GTG CAG 927
 GAA AAC TAC CTG GAG TAC CGG CAG GTC CCC GGC AGT GAT CCT 969
 GCA TGT TAT GAA TTC CTG TGG GGT CCA AGG GCC CTC GTT GAA 1011
 ACC AGC TAT GTG AAA GTC CTG CAC CAT ATG GTA AAG ATC AGT 1053
 GGA GGA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAG TGG GTT 1095
 TTG AGA GAG GGG GAA GAG TGA 1116
 GTCTGAGCAC GAGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT 1166
 GCACCTTCCG GGGCCGCATC CCTTAGTTTC CACTGCCTCC TGTGACGTGA 1216
 GGCCCATTTCT TCACTCTTTG AAGCGAGCAG TCAGCATTCT TAGTAGTGGG 1266
 TTTCTGTTCT GTTGGATGAC TTTGAGATTA TTCTTTGTTT CCTGTTGGAG 1316
 TTGTTCAAAT GTTCCTTTTA ACGGATGGTT GAATGAGCGT CAGCATCCAG 1366
 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGAG 1416
 TAAGAGTCTT GttTTTTACT CAAATTgGGA AATCCATTCC ATTTTGTGAA 1466
 TTGTGACATA ATAATAGCAG TGGTAAAAGT ATTTGCTTAA AATTGTGAGC 1516
 GAATTAGCAA TAACATACAT GAGATAACTC AAGAAATCAA AAGATAGTTG 1566
 ATTCTTGCCT TGTACCTCAA TCTATTCTGT AAAATTAAAC AAATATGCAA 1616
 ACCAGGATTT CCTTGACTTC TTTG 1640

(2) INFORMATION FOR SEQUENCE ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: genomic DNA

(ix) FEATURE:

- (A) NAME/KEY: MAGE-31 gene

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA CCCAGTAGA GTGGGGACCT CACAGAGTCT GGCCAACCCT 50
 CCTGACAGTT CTGGGAATCC GTGGCTGCGT TTGCTGTCTG CACATTGGGG 100
 GCCCGTGGAT TCCTCTCCCA GGAATCAGGA GCTCCAGGAA CAAGGCAGTG 150
 AGGACTTGGT CTGAGGCAGT GTCCTCAGGT CACAGAGTAG AGGGGgCTCA 200
 GATAGTGCCA ACGGTGAAGG TTTGCCTTGG ATTCAAACCA AGGGCCCCAC 250
 CTGCCCCAGA ACACATGGAC TCCAGAGCGC CTGGCCTCAC CCTCAATACT 300
 TTCAGTCCTG CAGCCTCAGC ATGCGCTGGC CGGATGTACC CTGAGGTGCC 350
 CTCTCACTTC CTCCTTCAGG TTCTGAGGGG ACAGGCTGAC CTGGAGGACC 400
 AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAAGCCTTTG 450
 TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCTCACATGC 500

TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCAGCT CCTGCCCACA	550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	622
GGC CTT GAG GCC CGA GGA GAg GCC CTG GGC CTG GTG GGT GCG	664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCC TCT	706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCT GCC	748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC ACC TTC	874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT AGG AAG	916
GTG GCC AAG TTG GTT CAT TTT CTG CTC	943

(2) INFORMATION FOR SEQUENCE ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1067 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(ix) FEATURE:

(A) NAME/KEY: cDNA MAGE-4

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGG CCA AGC ACC TCG CCT GAC GCA GAG TCC TTG TTC CGA	39
GAA GCA CTC AGT AAC AAG GTG GAT GAG TTG GCT CAT TTT CTG	81
CTC CGC AAG TAT CGA GCC AAG GAG CTG GTC ACA AAG GCA GAA	123
ATG CTG GAG AGA GTC ATC AAA AAT TAC AAG CGC TGC TTT CCT	165
GTG ATC TTC GGC AAA GCC TCC GAG TCC CTG AAG ATG ATC TTT	207
GGC ATT GAC GTG AAG GAA GTG GAC CCC GCC AGC AAC ACC TAC	249
ACC CTT GTC ACC TGC CTG GGC CTT TCC TAT GAT GGC CTG CTG	291
GGT AAT AAT CAG ATC TTT CCC AAG ACA GGC CTT CTG ATA ATC	333
GTC CTG GGC ACA ATT GCA ATG GAG GGC GAC AGC GCC TCT GAG	375
GAG GAA ATC TGG GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT	417
GGG AGG GAG CAC ACT GTC TAT GGG GAG CCC AGG AAA CTG CTC	459
ACC CAA GAT TGG GTG CAG GAA AAC TAC CTG GAG TAC CGG CAG	501
GTA CCC GGC AGT AAT CCT GCG CGC TAT GAG TTC CTG TGG GGT	543
CCA AGG GCT CTG GCT GAA ACC AGC TAT GTG AAA GTC CTG GAG	585
CAT GTG GTC AGG GTC AAT GCA AGA GTT CGC ATT GCC TAC CCA	627
TCC CTG CGT GAA GCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	669
TGAGCATGAG TTGCAGCCAG GGCTGTGGGG AAGGGGCAGG GCTGGGCCAG	719
TGCATCTAAC AGCCCTGTGC AGCAGCTTCC CTTGCCTCGT GTAACATGAG	769
GCCCATTCTT CACTCTGTTT GAAGAAAATA GTCAGTGTTT TTAGTAGTGG	819
GTTTCTATTT TGTTGGATGA CTTGGAGATT TATCTCTGTT TCCTTTTACA	869
ATTGTTGAAA TGTTCTTTT AATGGATGGT TGAATTAAT TCAGCATCCA	919
AGTTTATGAA TCGTAGTTAA CGTATATTGC TGTTAATATA GTTTAGGAGT	969
AAGAGTCTTG TTTTTTATTC AGATTGGGAA ATCCGTTCTA TTTTGTGAAT	1019
TTGGGACATA ATAACAGCAG TGGAGTAAGT ATTTAGAAGT GTGAATTC	1067

(2) INFORMATION FOR SEQUENCE ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs
- (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(ix) FEATURE:
 (A) NAME/KEY: MAGE-5 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AGGATCCCCA GGAGGCCCTA GAGGAGCACC AAAGGAGAAG ATCTGTAAGT 50
AAGCCTTTGT TAGAGCCTCC AAGGTTTCAGT TTTTAGCTGA GGCTTCTCAC 100
ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC TCCATTGCCC AGCTCCTGCC 150
CACACTCCTG CCTGTTGCGG TGACCAGAGT CGTC 184
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA 226

(2) INFORMATION FOR SEQUENCE ID NO: 15:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 225 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:
 (A) NAME/KEY: MAGE-6 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

TAT TTC TTT CCT GTG ATC TTC AGC AAA GCT TCC GAT TCC TTG 42
CAG CTG GTC TTT GGC ATC GAG CTG ATG GAA GTG GAC CCC ATC 84
GGC CAC GTG TAC ATC TTT GCC ACC TGC CTG GGC CTC TCC TAC 126
GAT GGC CTG CTG GGT GAC AAT CAG ATC ATG CCC AGG ACA GGC 168
TTC CTG ATA ATC ATC CTG GCC ATA ATC GCA AGA GAG GGC GAC 210
TGT GCC CCT GAG GAG 225

(2) INFORMATION FOR SEQUENCE ID NO: 16:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(ii) MOLECULE TYPE: genomic DNA
(ix) FEATURE:
 (A) NAME/KEY: MAGE-7 gene
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACA AGC ACT AGT TTC CTT GTG ATC TAT GGC AAA GCC TCA GAG 42
TGC ATG CAG GTG ATG TTT GGC ATT GAC ATG AAG GAA GTG GAC 84
CCC GCG GCC ACT CCT ACG TCT TGT ACC TGC TTG GGC CTC TCC 126
TAC AAT GGC CTG CTG GGT GAT GAT CAG AGC ATG CCC GAG A 166